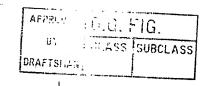
DRAFTSIA

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><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

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Signal peptide: amino acids 1-24

N-glycosylation sites: amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites:

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 26-30

Casein kinase II phosphorylation sites:

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343 and 349-353

Tyrosine kinase phosphorylation site: amino acids 303-310

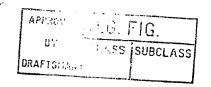
N-myristoylation sites:

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and 313-319

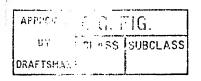
Aspartic acid and asparagine hydroxylation site: amino acids 308-320

EGF-like domain cysteine pattern signature: amino acids 166-178

Leucine zipper pattern: amino acids 94-116



CAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGAŢĊCCTC GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCCCCAGCCGTCTAAAGGGGAACA GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGCCCGGAGGÃ CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCĞĞAGGC CGGGCCGCCGCAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCCTGTCAATATCCATTCCATGAATTTTAC CTGGCAAGCTGCAGGGCAGAATACTTCTATGAATTCCTGTCCTTGCGCTCCCTGGATA AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTTGAAGT GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCCAAAACACCTCAAAATGCTATCT TCTTTAAAACATGTCAACAAGCTGAGTGCCCAGGCGGTGCCGAAATGGAGGCTTTTGTAAT GAAAGACGCATCTGCGAGTGTCCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG TACCCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCCACCTG GATTCTATGGAGTGAACTGTGACAAAGCAAACTGCTCAACCACCTGCTTTAATGGAGGGACC TGTTTCTACCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG CAAATGCCCACAACCCTGTCGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTT CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACAT GGAACCTGCCATGAACCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCCAGCTCAGGCAGC ACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGG TGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTCA TGTGTTGAATGTTCAAATAATGTTCATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT TCATTATAAATCACTGAGCTGATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGTCTGTAG CATGATGGTATAGATTTTCTTGTTTCAGTGCTTTTGGGACAGATTTTATATTATGTCAATTGA TCAGGTTAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAAATTACAATGCATTTATGGT GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAAT TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGATTTTATTGTCAGATATTTAGAT GTTTGTTACATTTTTAAAAATTGCTCTTAATTTTTAAACTCTCAATACAATATATTTTGACC AAACAATATAAŢATATTCTAAACACAATGAAATAGGGAATATAATGTATGAACTTTTTGCAT TGGCTTGAAGCAATATAATATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTAT AAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC CGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG



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><subunit 1 of 1, 379 aa, 0 stop

><MW: 41528, pI: 7.97, NX(S/T): 2

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GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW

Signal peptide: amino acids 1-28

N-glycosylation site: amino acids 88-92, 245-249

Casein kinase II phosphorylation site: amino acids 319-323

Tyrosine kinase phosphorylation site: amino acids 370-378

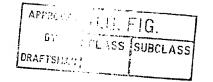
N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

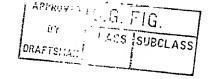
ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature: amino acids 198-210, 230-242, 262-274, 294-306, 326-338



CCCCAGCCCACACCTTCACCAGGGCCCAGGAGCCACCATGTGGGCGATGTCCAGTGGGGCTAC TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGG GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA GCAGGACCTGTGCTGCCGCGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCCCTGACTTCTGGGACTTC TGCCTCGGCGTGCCACCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA TCCAGTCTTGGGAACGTACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT GAACCACAGCGCCTTCTGGGGCATGACCCTGGA**TGA**GGGCATTCGCTACCGCCTGGGCACCA TCCGCCCATCTTCCTCGGTCATGAACATGCATGAAATTTATACAGTGCTGAACCCAGGGGAG GTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGA CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT CAATCCATTCTCTGGGACACATGACGCCTGTCCTGTCGCCCCAGAACCTGCTGTCTTGTGAC ACCCACCAGCAGGAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCG CCGAGGGTGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTCGGGGCAAGCGCCAGGCCACTGCC CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA TGGAGGTGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGAG AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCATCACTGAGGCTG CGGGCACCACGCGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCCAATG GGGCGGTGACCCCAGCCTCGCCCGACAGAGCCCGGGGCGCAGGCGCGCCAGGGCGCTAAT CCCGGCGCGGGTTCCGCTGACGCAGCGCCCCGCCTGGGAGCCGCGGGCAGGCGAGACTGGCG GAGCCCCCAGACCTCCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG ATCCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC TTGCCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA AGTGACCCTCCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACCACCTGGC TAATTTTTGTATTTTTTTTGTAAAGAGGGGGGTCTCACTGTGTTTGCCCAGGCTGGTTTCGAACT CCTGGGCTCAAGCGGTCCACCTGCCTCCCCAAAGTGCTGGGATTGCAGGCATGAGCC TAAAACCAAAGTATTGATAAAAAAAAA



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><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

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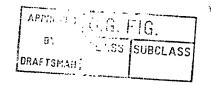
N-glycosylation site: amino acids 78-82, 161-165

Casein kinase II phosphorylation site: amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300, 411-415

N-myristoylation site: amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230, 269-275, 378-384, 442-448

Amidation site: amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site: amino acids 398-409



AGGCTCCTTGGCCCTTTTTCCACAGCAAGCTTNTGCNATCCCGATTCGTTGTCTCAAATCCA

ATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC

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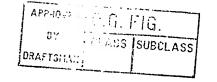
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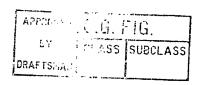
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TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG

AGGCCAGAGAGAGATACCGCCGGCATGGGACCCACTCAG



GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGCTACT CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCAGĆĈAĞCTGGĞG GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCCAAAGGCTG CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAAGATCACGTGCT GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT GCGCTGCTCCCTGCACTCGGCCTGCTGCTGCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG CTGCACCCTGTCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCTCCAACCCTCTCTGCTGCTGTTTC CATGGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT CCCTGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA GGGGACAGGCACTCAGGAGGGCCCAG**TAA**AGGCTGAGATGAAGTGGACTGAGTAGAACTGGA GGACAAGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA GGGGCCAGGCCTCACATTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT AATAAACACCTGTTGGATAAGCCAAAAAA



MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPTLGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSSDTDPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide: amino acids 1-47

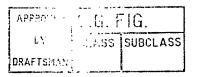
N-glycosylation site: amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site: amino acids 22-26,

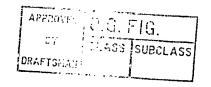
76-80

N-myristoylation site: amino acids 56-60

Amidation site: amino acids 70-74



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MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHYQVTGRRI SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLE NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF VGSAPTRRTKRTRRPQPLT

Signal peptide: amino acids 1-22

N-glycosylation site: amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 60-64

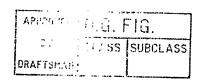
Casein kinase II phosphorylation site: amino acids 65-69

Tyrosine kinase phosphorylation site: amino acids 39-48, 89-97

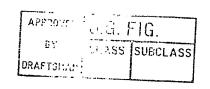
N-myristoylation site: amino acids 69-75, 188-194

Amidation site: amino acids 58-62

HBGF/FGF family signature: amino acids 103-128



ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAĞ GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT TTCCGTACTTCAGAA**ATG**GGCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCCT GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC CTAGTGTGTGCCGCTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACCAAACTTAATAATGC TGGATTTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC AACTGGACGAATTCCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAC AATATTCAGACCATTTCACGGGCTGCTCTTGCCCAGCTCTTGAAGCTTGAAGAGCTGCACCT GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCC TCAAATTGTTTTTTTTTTTTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCCTGTGGAC TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCATATCCGACATGGCCTTCCAGAA TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC CACCCTCCCGATCTCCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC ACTGCTCGGAATAACCCTTGGTTTTGTGACTGCAGTATTAAATGGGTCACAGAATGGCTCAA ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCCTGAACAAGTCCGGG GGATGGCCGTCAGGGAATTAAATATGAATCTTTTGTCCTGTCCCACCACGACCCCCGGCCTG CCTCTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACCTCAGCCTCCCACCCTCTCTAT TCCAAACCCTAGCAGAAGCTACACGCCTCCAACTCCTACCACATCGAAACTTCCCACGATTC CTGACTGGGATGGCAGAAAGAGTGACCCCACCTATTTCTGAACGGATCCAGCTCTCTATC CAAACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGGCATCGTTCAGGAGCGCATAG TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTCAGAGGC CACCACCCATGCCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGGCTTGATCGGGGGGCGCGGTGATATTT GTGCTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATATGCACAAAAAGGGGCGCTACACCTC AGGACAACTCCATCCTGGAGATGACAGAAACCAGTTTTCAGATCGTCTCCTTAAATAACGAT CACAGACTGCCATATCCCCAACAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC ACTGCCATACG**TGA**CAGCCAGAGGCCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAAGTG CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACTCTTTGCTTTTTAAATCTT



MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
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SRAALAQLLKLEELHLDDNSISTVGVEDGAFREAISLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCQGPEQVRGMAVRELNMNLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide: amino acids 1-42

Transmembrane domain: amino acids 542-561

N-glycosylation site: amino acids 202-206, 298-302, 433-437,

521-525, 635-639, 649-653

Casein kinase II phosphorylation site: amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site: amino acids 319-328

N-myristoylation site: amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300, 522-528, 545-551, 633-639

Amidation site: amino acids 581-585

Leucine zipper pattern: amino acids 164-186

Phospholipase A2 aspartic acid active site: amino acids 39-50

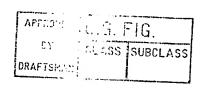


FIGURE 14A

ACTTGGAGCAAGCGGCGGCGGGGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCTCG CCTCCCACGAGCGATCCCCGAGGAGAGCCGCGCCCTCGGCGAGGCGAAGAGGCCGAGGAGG AAGACCCGGGTGGCTGCCCTGCCTCGCTTCCCAGGCGCCGGCGGCTGCAGCCTTGCCCC TCTTGCTCGCCTTGAAA**ATG**GAAAAGATGCTCGCAGGCTGCTTTCTGCTGATCCTCGGACAG ATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTCACGTGGGAGGTCCATCTCTAGGGGCAG ACACGCTCGGACCCACCCGCAGACGGCCCTTCTGGAGAGTTCCTGTGAGAACAAGCGGGCAG ACCTGGTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCCATGACTATGCAAAGGTCAAG GAGTTCATCGTGGACATCTTGCAATTCTTGGACATTGGTCCTGATGTCACCCGAGTGGGCCT GCTCCAATATGGCAGCACTGTCAAGAATGAGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCG AGGTGGAGCGTGCTGAAGAGGATGCGGCATCTGTCCACGGGCACCATGACTGGGCTGGCC ATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCCGGCCCCTGAGGGAGAA TGTGCCACGGGTCATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGG CTGCTAAGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTC AACACCTTGAAGTCCATTGGGAGTGAGCCCCATGAGGACCATGTCTTCCTTGTGGCCAATTT CAGCCAGATTGAGACGCTGACCTCCGTGTTCCAGAAGAAGTTGTGCACGGCCCACATGTGCA GCACCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTGGCTCATACGTCTGCAGG TGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGTGTGC CATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGT GCTACAGTGGCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCC TCAGAAAACCACGGATGTGAACATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTG CCATGAAGGATTTGCTCTTAACCCAGATGAAAAAACGTGCACAAGGATCAACTACTGTGCAC TGAACAAACCGGGCTGTGAGCATGAGTGCGTCAACATGGAGGAGAGCTACTACTGCCGCTGC CACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCACA GCAGGACCATGGCTGTGAGCAGCTGTCTGAACACGGAGGATTCCTTCGTCTGCCAGTGCT AGTGACCATGGTTGTGAATACTCCTGTGTCAACATGGACAGATCCTTTGCCTGTCAGTGTCC TGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTGCAAAATTGGACTCTTGTGCTCTGG GGGACCACGGTTGTGAACATTCGTGTGTAAGCAGTGAAGATTCGTTTTGTGTGCCAGTGCTTT GAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTAT AGACCATGGCTGTGAACACTTTGTGTGAACAGTGACGACTCATACACGTGCGAGTGCTTGG

To Figure 14B

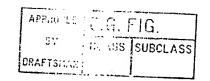
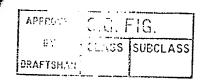


FIGURE 14B

From Figure 14A

CACCATGGCTGCGAACACATTTGTGTTAATAATGGGAATTCCTACATCTGCAAATGCTCAGA GGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAATTGCACTGAAGGCCCAÁTT.GACC TGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTCGTGAAGCAG TTTGTCACTGGAATTATAGATTCCTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGĞCTGCT CCAGTATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCCAAAGACA TGAAAAAAGCCGTGGCCCACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTG AAACACATGTTTGAGAGAAGTTTTACCCAAGGAGAAGGGGCCAGGCCCCTTTCCACAAGGGT GCCCAGAGCAGCCATTGTGTTCACCGACGGACGGGCTCAGGATGACGTCTCCGAGTGGGCCA GTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTGAGGAG GAACTACAAGAGATTGCCTCTGAGCCCACAAACAAGCATCTCTTCTATGCCGAAGACTTCAG CACAATGGATGAGATAAGTGAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCG ATGGAAGACAGGACTCTCCAGCAGGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCT GAGCCAGTCACCATAAATATCCAAGACCTACTTTCCTGTTCTAATTTTGCAGTGCAACACAG ATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTTCCCCATTCAACAAAAC CTTCAGGAAGCCCTTTGGAAGAAAACACGATCAATGCAAATGTGAAAACCTTATAATGTTC CAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAG AATGGAAGCCCTGGAAAATCGCCTGAGATACAGA**TGA**AGATTAGAAATCGCGACACATTTGT AGTCATTGTATCACGGATTACAATGAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTA AATCAATAATGTTGTGAAGTAAAACAATCAGTACTGAGAAACCTGGTTTGCCACAGAACAA GACAAGAAGTATACACTAACTTGTATAAATTTATCTAGGAAAAAAATCCTTCAGAATTCTAA GATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAATATACTGTGGACA CAACTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTT ACCTTGATATATGTATATGGATGTATGCATAAAATCATAGGACATATGTACTTGTGGAACAA GTTGGATTTTTTATACAATATTAAAATTCACCACTTCAG



MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPQTALLESSCENKRADLVFLIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV KRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGC EHECVNMEESYYCRCHRGYTLDPNGKTCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGCE HSCVSSEDSFVCQCFEGYILREDGKTCRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA EDGKRCRKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN GITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTORMEALENRLRYR

Signal peptide: amino acids 1-23

N-glycosylation site: amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site: amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247, 401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784, 781-785, 819-823, 866-870

N-myristoylation site: amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500, 639-645, 690-696, 752-758, 792-798

Amidation site: amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site: amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464, 540-546, 581-587

APPRIONE CLASS SUBCLASS
BRAFTSMAR

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGCAGCCTCG CATGATTTCCCTCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA GCGGTGGAGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGAGGTGTCTTC AGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC ATGCCCTCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCCACAGCATCAAAACCT TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCCAC AATGAGGTGGCCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAACGATGATATCAAGGAGGATGCC ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT TTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT TGACCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGAT GGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG CATGGGTGCTGTGCTGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTA**TGA**TGAC AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCCACCTCTC TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGA AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCTGACTCCTTATGAAGCCAGCTG CTGAAATTAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGC CCCCTTGATCTGTACCCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC **TGTTTGTATGAAAA**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKSSDTISKNGTL SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR MGAVPVMVPAQSQAGSLV

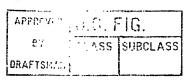
Signal peptide: amino acids 1-29

Transmembrane domain: amino acids 245-267

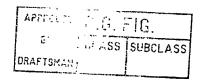
N-glycosylation site: amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site: amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262, 262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 164-175



CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCCGCTCCTAGTGGTTTTTTTCCACTTTG TTGAATTGTTCCTATACTCAAAATTGCACCAAGACACCTTGTCTCCCAAATGCAÁAATGTGA AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTCACAA TTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGTCCTGTGGCGAAAATĜCTÄATTĠC ACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCAGCAGTAACCA. AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATT TAGATAATGTCTGTATAGCTGCAAATATTAATAAAACTTTAACAAAAATCAGATCCATAAAA GAACCTGTGGCTTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTTCACCAACAGA TATAATTACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAACA CTATCTCAGCCAAGGACACCCTTTCTAACTCAACTCTTACTGAATTTGTAAAAACCGTGAAT AATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAAC ACATCTTACAAAACTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC AAAAGACCACAGAGTTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTTCTTTTTTGAT TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATA AGAGTATTGGTCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGAT AATTCTGAAGAGGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC ACCCACATTATATGAACTTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATA GGTATAGGAGTCTATGTGCATTTTGGAATTACTCACCTGATACCATGAATGGCAGCTGGTCT TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT GACACATTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTC TTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTT ACCTTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCTG TAGCCTATTTCTTGCTGAACTTGTTTTTCTTGTTGGGATCAATACAAATACTAATAAGCTCT TCTGTTCAATCATTGCCGGACTGCTACACTACTTCTTTTTAGCTGCTTTTTGCATGGATGTGC ATTGAAGGCATACATCTCTATCTCATTGTTGTGGGTGTCATCTACAACAAGGGATTTTTGCA CAAGAATTTTTATATCTTTGGCTATCTAAGCCCAGCCGTGGTAGTTGGATTTTCGGCAGCAC TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAACAACTTTATT TGGAGTTTTATAGGACCAGCATGCCTAATCATTCTTGTTAATCTCTTGGCTTTTTGGAGTCAT TAAGGTCTTGTGCAAGAGGGCCCTCGCTCTTCTGTTCCTTCTCGGCACCACCTGGATCTTT GGGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTTCACAGTCAGCAATGC ATTACAGATTGTTCAAAAATGTCCCCTGTTGTTTTTGGATGTTTAAGG**TAA**ACATAGAGAATG GTGGATAATTACAACTGCACAAAAATAAAAATTCCAAGCTGTGGATGACCAATGTATAAAAA TGACTCATCAAATTATCCAATTATTAACTACTAGACAAAAAGTATTTTAAATCAGTTTTTCT GTTTATGCTATAGGAACTGTAGATAATAAGGTAAAATTATGTATCATATAGATATACTATGT TTTTCTATGTGAAATAGTTCTGTCAAAAATAGTATTGCAGATATTTGGAAAGTAATTGGTTT TGTCCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTTGCCTTTGAAACTAGTCC CCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGCAGA TAGCTGAGAAATTGTTGACATAAAATAAAGAATTGAAGAAACACATTTTACCATTTTGTGAA TTGTTCTGAACTTAAATGTCCACTAAAACAACTTAGACTTCTGTTTGCTAAATCTGTTTCTT



MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSSLLGYKNNTISAKDTL
SNSTLTEFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISOSFQKTTEFDT,
NSTDIALKVFFFDSYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYSPDTMNGSWSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSIIAGL
LHYFFLAAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide: amino acids 1-19

Transmembrane domain: amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636, 648-664

N-glycosylation site: amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181, 188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site: amino acids 49-53

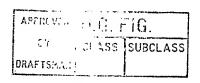
cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 360-364

Casein kinase II phosphorylation site: amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154, 155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329, 346-350, 608-612

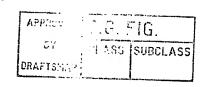
Tyrosine kinase phosphorylation site: amino acids 36-44, 669-677, 670-678

N-myristoylation site: amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394, 434-440, 480-486, 521-527

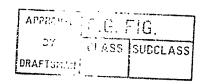
Aspartic acid and asparagine hydroxylation site: amino acids 75-87



TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCCCACC
ATTATATGAACTTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATTTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTTGCCATATGCATTTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA



GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCCGGCCG CTAAGCGAGGCCTCCTCCCCCCAGATCCGAACGGCCTGGGCGGGTCACCCÉGGCTGGGA CAAGAAGCCGCCGCCTGCCCGGGCCCGGGGAGGGGCTGGGGCTGGGGCCGGAGGCGG GGTGTGAGTGGGTGTGTGCGGGGGGGGGGGGGTTGATGCAATCCCGATAAGAAATGCTCGGG TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG $\verb|CCGCCGCGCCGTCAGAGCAGGAGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC|\\$ GGCACTCACAGCCCCGCAGCGCATCCCGGTCGCCGCCCAGCCTCCCGCACCCCCATCGCCGG AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG ATCCTGGCCGGCCTCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGCC CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC ACGGGCTCTCCAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGGC CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG CGTGCACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT ACTCGGAGGAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA CAGAGGCTTTCTTCCACTCTCATTTCCTGCCCATGCTCCCATGGTCCCAGAGGAGCCTG AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCTGGAGACCGACAGCATG GACCCATTTGGGCTTGTCACCGGACTGGAGGCCGTGAGGAGTCCCAGCTTTGAGAAG**TAA**CT GAGACCATGCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGGCTTTAGGAAGAACATCTAGAA GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT CATAACATTGTAAGCCTGTAGCTTGCCCAGCTGCTGCCTGGGCCCCCATTCTGCTCCCTCGA GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCATTGAATACCTCCATCGATGGGGAAC TCACTTCCTTTGGAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTCAGGAACAGGTGATCCACTCTGTA AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC CTGAGGCCAGTTCTGTCATGGATGCTGTCCTGAGAATAACTTGCTGTCCCGGTGTCACCTGC TTCCATCTCCCAGCCCACCAGCCCTCTGCCCACCTCACATGCCTCCCCATGGATTGGGGCCT CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC TTTTGTATATTAAAATGGAGTTTGTTTGT



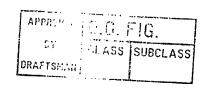
MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide: amino acids 1-22

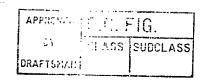
Casein kinase II phosphorylation site: amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site: amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 48-59



CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCTÈA GAGCAGCCGGCTGCCGCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG CTGCTGCGCTGCTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA AGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAAACTGGGTCGGAGTGTCTCCTTTGTCTAC TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAACT CTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG CCGCGGCGGCGGATCACGAGGTCAGGAGTTC**TAG**ACCAGTCTGGCCAATATGGTGAAACCC CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC



MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAAGGSRGQ
EF

Signal peptide: amino acids 1-20

Transmembrane domain: amino acids 130-144, 238-258

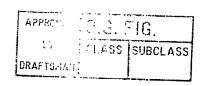
N-glycosylation site: amino acids 98-102, 187-191, 236-240,

277-281

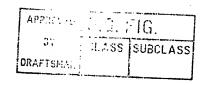
Casein kinase II phosphorylation site: amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site: amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site: amino acids 226-230



GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAGGAGGAGGAGAAAGAG AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCAT CATGCTGCTATTCCTGCAAATACTGAAGAAGCATGGGATTTAAATATTTTACTTGTAAATAA ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA TTATATCATTAAGGAAATAGTAACCTTCTCTCTCCCAATATGCATGACATTTTTGGACAATG CAATTGTGGCACTGGCACTTATTTCAGTGAAGAAAACTTTGTGGTTCTATGGCATTCATCA TGGAATCCTTAAGGGCCCATTACATTTCTGAAGAAGAAGCTAAGATGAAGGACATGCCACT CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT AGCTAACACACAGATTCTTCTCCTACAGACTAACAATATTGCAAAAATTGAATACTCCACAG ACTTTCCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAAT ACTGCCTGAAAAATGTCTGTCCGAACTGAGCAACTTACAAGAACTCTATATTAATCACAACT TGCTTTCTACAATTTCACCTGGAGCCTTTATTGGCCTACATAATCTTCTTCGACTTCATCTC AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAGAGAT TCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACTTTAAGCCTCTTATCA ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT GGACTGGAAAACTTAGAAAGCATCTCTTTTTACGATAACAGGCTTATTAAAGTACCCCATGT GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC TACTAACAACCCTAGATTGTCTTACATTCACCCCAATGCATTTTTCAGACTCCCCAAGCTGG AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCATCCGTTG GATGAACATGAACAAAACCAACATTCGATTCATGGAGCCAGATTCACTGTTTTGCGTGGACC CACCTGAATTCCAAGGTCAGAATGTTCGGCAAGTGCATTTCAGGGACATGATGGAAATTTGT CTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT TTCCTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTTCTG GTCAAAAACTCTTGCCTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA GATATAAATGGCGTAACTCCCAAAGAAGGGGGGTTTATATACTTGTATAGCAACTAACCTAGT GCTCTTTGAATATTAAAATAAGAGATATTCAGGCCAATTCAGTTTTGGTGTCCTGGAAAGCA AGTTCTAAAATTCTCAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAATTCTCA TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC CATCAACTGAGTATAAAATTTGTATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAAA TGTGTAAATGTCACCACCAAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC CACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGGATTATTGGTGTGATATGTCTTATCA AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA ${\sf AGAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCC}{f T}$ **AA**AAACCACCAAGGAAACCTACTCCAAAAATGAAC



MKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLLQTNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
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IKVPHVALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence: amino acids 1-22

Transmembrane domain: amino acids 633-650

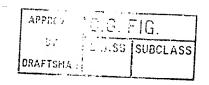
N-glycosylation site: amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583, 608-612, 624-628, 625-629

Casein kinase II phosphorylation site: amino acids 51-55, 95-99, 242-246, 468-472, 487-491

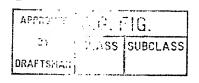
Tyrosine kinase phosphorylation site: amino acids 570-579

N-myristoylation site: amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443, 491-497, 492-498, 634-640, 702-708

Cell attachment sequence: amino acids 277-280



GCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG CTGCAGCCTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTC GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCCTCAATGCTGC CAACGACGCTGACCTTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG ACCTGATGATATTAGCACTGTGGTA**TAG**TGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTTCTGAGT ACA



MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL
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Signal sequence: amino acids 1-33

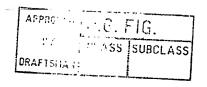
Transmembrane domain: amino acids 205-220

N-glycosylation site: amino acids 47-51, 94-98

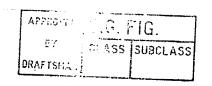
cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 199-203

Casein kinase II phosphorylation site: amino acids 162-166, 175-179

N-myristoylation site: amino acids 37-43, 45-51, 110-116



ACCGAGCCGAGCGGACCGAAGGCGCCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG GGCGTGAGGAGCATGCCCAGCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCGCCAG CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAĞCCCGGCG CCTTCAACCACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGCACGGCCT CATCGTCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCCTCAACCTCTCCTACAACCCCATCA GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCCTGTGGGTGTTCCGG CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCCACGTGCGCCACGCCCGAGTTTGTCCA GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACCTGCCGCCGC CCCGCATCCGGGACCGCAAGGCCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT GTGTGCCGGGCCGATGGCGACCCGCCGCCATCCTCTGGCTCTCACCCCGAAAGCACCT GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT TCCATGCCCGCCCACCTGCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAA GACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG TGCCTTTCCCCTTCGACATCAAGACCCTCATCATCGCCACCATGGGCTTCATCTCTTTC CTGGGCGTCGTCTTCTGCCTGGTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC AAAGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG ACGCGCCCGCAAGTTCAACATGAAGATGATA**TGA**GGCCGGGGGGGGGGGGGACCCCCG GGCGGCCGGCAGGGGAAGGGGCCTGGTCGCCACCTGCTCACTCTCCAGTCCTTCCCACCTC CTCCCTACCCTTCTACACACGTTCTCTTTCTCCCTCCCGCCTCCGTCCCCTGCTGCCCCCG CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA ATAATTCAATAAAAAGTTACGAACTTTCTCTGTAACTTGGGTTTCAATAATTATGGATTTT



MQVSKRMLAGGVRSMPSPLLACWQPILLLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELELNENIVSAVEPGAFNNLFNERTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGNLETLILDSNPLA
CDCRLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
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Signal sequence: amino acids 1-41

Transmembrane domain: amino acids 556-578

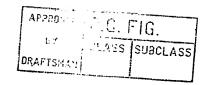
N-glycosylation site: amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345, 492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site: amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353, 607-611

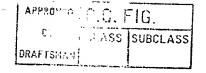
Tyrosine kinase phosphorylation site: amino acids 590-598

N-myristoylation site: amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143, 262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 32-43



CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCCGGGGATTCAGGCTCGCCAGCGCCAGCC AGGGAGCCGGCCGGAAGCGCGATGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC ACATCTGATGAAACAGTGGTGGCTGGTGCCACCGTGGTGCTCAAGTGCCAAGTGAAAGATCA CGAGGACTCATCCCTGCAATGGTCTAACCCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA GAGCCCTTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTT ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAG ACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT GCCCTGATCTTCCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCT CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCCTGCTG TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG ${\tt GGCAGTCAGGAGGGACGACAAGAAGGAATATTTCATC} {\bf TAG} {\tt AG} {\tt AGGCGCCTGCCCACTTCCTGC}$ GCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTCACCAACCCGGACTTGTACAGAGCAA CCGCAGGCCCCCCCCCCTCCCCCTTGCTCCCCAGCCCACCCCCCCTGTACAGAATGTCTGC TTGCCCTCAGCCCTTTCCGTGGCTTCTCTGCATTTGGGTTATTATTATTTTTTGTAACAATCC AACAAAAAACA



MGAPAASLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSISISNVALADEGEYTCSIFTMPVRTAKSLV TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence: amino acids 1-20

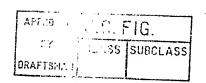
Transmembrane domain: amino acids 331-352

N-glycosylation site: amino acids 25-29, 290-294

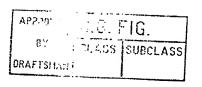
Casein kinase II phosphorylation site: amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site: amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304, 306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 7-18



GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCTTTTCTTCTCCTTGG CTTCGGACATTGGAGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAA**TG**CTGCTTTGGATŢCŦGTT TCTGTTCCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG AAAACAATGGCTTGCATGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG CTGCACATCAACAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTĠĞACGA TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCCTTCCAGG ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCTACCTGCCAAC GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCC CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC CACCGAACAGGACTTGTGTCCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG CCCAAGAAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACA GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCCAGGGTCGGGTTTAAAGATGAAC TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA GCTTTTCCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA ACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAAG AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA TCCTCCCGGGCACTTTCAATGCCATGCCCAAACTGAGGATCCTCATTCTCAACAACAACCTG CTGAGGTCCCTGCGGGCTGTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA CAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACTTCTT TAGAAAGGATTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT CGCCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGGACGCACTCC AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGGT GTTTGTCACCTCCGCCTTCACCGTGGTGGGGCATGCTCGTGTTTATCCTGAGGAACCGAAAGC GACTCTTCCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCCACAGAGTGTATGACTG TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG ATACATCCTTCCCCACCGCAGGCACCCCGGGGGGCTGGAGGGGGCGTGTACCCAAATCCCCGCG CCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTCGCACAACCGAAAGGGCCT GACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA GCCAGCTCGCTCTTTGCTGAGAGCCCCTTTTGACAGAAAGCCCAGCACGACCCTGCTGGAAG AACTGACAGTGCCCTCGCCCTCGGCCCCGGGGCCTGTGGGGTTGGATGCCGCGGTTCTATAC ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCCTGTGGATTAG CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT TGTAAATAAGTAACTTTGACTTCTGAC



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VPGLLLVFVTSAFTVVGMLVFILRNRKRSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG
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Signal sequence: amino acids 1-15

Transmembrane domain: amino acids 618-638

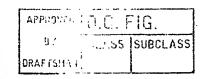
N-glycosylation site: amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 122-126, 646-650

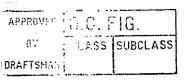
Casein kinase II phosphorylation site: amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577, 608-612, 657-661, 666-670, 693-697

N-myristoylation site: amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349, 354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 337-348



AGTCGACTGCGTCCCTGTACCCGGCGCCAGCTGTGTTCCTGACCCCAGAATAACTCAGGGC TGCACCGGGCCTGGCAGCGCTCCGCACACTTTCCTGTCGCGGCCTAAGGGAAACTGTTGGC CGCTGGGCCCGCGGGGGATTCTTGGCAGTTGGGGGGTCCGTCGGGAGCGAGGGCGGAGGGG AAGGGAGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC AGA**ATG**AGGCCGGCGTTCGCCCTGTGCCTCTCTGGCAGGCGCTCTGGCCCGGGCCGG CGGCGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTGC ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC AGCACCGTGCGTGCGGCCCGAGCTGCGCGCTGTGCTCCCTGCGGGCAGGCCCAGG GCCCGGAGGGGCTCCAAAGACCTGCTGTTCTGGGTCGCACTGGAGCGCAGGCGTTCCCACT GCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCCTCCGACCCCGGCGGTCTC GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC GGTACTCCAGGCCACCGGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC GCGCCAACGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCCTGCGCCGCCCCCGGG GCCGCCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG TCCACCTGGGACCGAGGTGAGTGCGCTCTGCCGGGGACAGCTCCCGATCTCAGTTACTTGCA TCGCGGACGAAATCGGCGCTCGCTGGGACAAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG CTTTGCCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA GCAACCAGCCCCGTGCCGCAGAGAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC ACCACTTGTCCCTGAACAAGACAATTCAGTAACATCTATTCCTGAGATTCCTCGATGGGGAT CACAGAGCACGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTT CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTTGGTGATCT TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCCTCTTCCCAGCCA AGGAAGGAGTCTATGGGCCCGCCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG CAGAGGGTGCCTTGCTGGCGGAGTCCCCTCTTGGCTCTAGTGATGCA**TAG**GGAAACAGGGGA CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACTTAC TTGTGTAACTGACAATTTCTGCAGAAATCCCCCTTCCTCTAAATTCCCTTTACTCCACTGAG GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGA TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGGAGAA TTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATATAATTTACA TTAAAAAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTCAGGCTAGGAGTAT ATTGGTTCGAAATCCCAGGGAAAAAAATAAAAATAAAAATTAAAGGATTGTTGAT



MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence: amino acids 1-16

Transmembrane domain: amino acids 399-418

N-glycosylation site: amino acids 189-193, 381-385

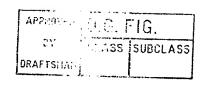
Glycosaminoglycan attachment site: amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 98-102, 434-438

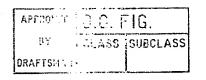
Casein kinase II phosphorylation site: amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site: amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157, 185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469, 477-483

Aspartic acid and asparagine hydroxylation site: amino acids 262-274



CGGACGCGTGGGATTCAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCÇGCGTATC CCCCGGCTACCTGGGCCGCCCCGCGGCGTGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA GCGCCGGTGTGAGCCAGCGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGTGCGGA GGGGCGTGTGTGCCGCCGCGCGCCGTGGGGTGCAAACCCCGAGCGTCTACĞCTGCC**ATG**A CAGCAGTCCCCAGAGAGCCTGTTTTCACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT TATTGGCAGTGAAGGTTTTCCTGGAGTGTACCCTCCAAATAGCAAATGTACTTGGAAAATCA CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTCATAGACCTCGAGAGTGACAAC CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA TGATTTCTGATGCCAACACACTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAAC CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC CGATATGATTATGTGGCTGTTTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTCAGT TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA AAACTGCCTACAACTACAGAACAGCCTGTCACCACCACATTCCCTGTAACCACGGGTTTAAA GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTCAGCAGGCGGG CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG TTAACAGTGAACTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTC TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT TGCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCGGTGATAGGA ATTTTAGAATTGAGTTGTGAAGATGTCAAAAAAAGATTTTAGAAGTGCAATATTTATAGT GTTATTTGTTTCACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTTCTA



MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence: amino acids 1-23

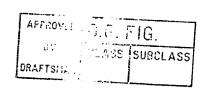
N-glycosylation site: amino acids 355-359

Casein kinase II phosphorylation site: amino acids 64-68, 142-146, 274-278

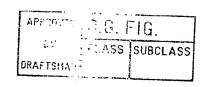
Tyrosine kinase phosphorylation site: amino acids 199-208

N-myristoylation site: amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295, 305-311, 309-315, 320-326, 330-336

Cell attachment sequence: amino acids 149-152



CGGACGCGTGGGCGGCCGGGCCCACGGCGCCCGCGGGCTGGGGCGGTCGCTTCTT CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGCCCCCATGGCCCCCGAAGG GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGG CTCCAGCCCTCTCCACCTCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACTTTGGAG GTGGAAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT GAGTGAGGAGCTGGTGGAGAGCTGGTTTCACAAGCAGCAGGAGGCCCCGGACCTCTTCC AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGCCCTCCTGC CTTCCCTGTCCTGGGGGAACAGAGGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG GACACGAGGGGCAGCGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCATCTGGTATGTTCGGCTTGT TTTGGCCCCTGTGCCCGATGCTCAGGACCTGAGGAATCAAACTGTTTGCAATGCAAGAAGGG CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG GCCTGCCTAGGCTGCATGGGGGCCAGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC AGAAGACGAGTTGGTGGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGGCTGTGGCGGCCATG ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCCTTCATCAAGGGCAGA**TA** ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCAGAGCTTGGGCTGCCC TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTG CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCCTGGGGTAAAAAGTAGC CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA ATTTCAAAAGTTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCCTGCTTAGGATTAGGTG GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT



MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence: amino acids 1-29

Transmembrane domain: amino acids 372-395

N-glycosylation site: amino acids 79-83, 205-209

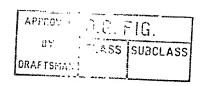
cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 290-294

Casein kinase II phosphorylation site: amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

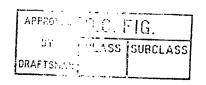
N-myristoylation site: amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179, 177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289, 326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site: amino acids 321-333

EGF-like domain cysteine pattern signature: amino acids 181-193



TGAGACCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA GCACCATGCAGCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCCTGGCCAGCCCCGGG GCCGCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCGGCAGCTGCAGCTCAAAGAGGT ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTCAGCCAGAGC TTCCGAGAGGTGGCCGGCAGGTTCCTGGCGTTGGAGGCCAGCACACCTGCTGGTGTTCGG CATGGAGCAGCGGCTGCCGCCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGCTGTCCCCGCGCAGCGCCCGGGCC CTCCAGGCTGGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA ACTTCTGGCAGCAGCCGGCCCCGGCAGCCGCTGCTACAGGTGTCGGTGCAGAGG GAGCATCTGGGCCCGCTGCGTCCGCGCCCACAAGCTGGTCCGCTTTGCCTCGCAGGGGGC GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG CTCAGGGCGACTGTGACCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCCGGGCTT CCTGGCTTATGAGTGTGGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC ATCAAGGAGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCAGAA GTGCAGCTGTGCCTCGGATGGTGCGCTCGTGCCAAGGAGGCTCCAGCCA**TAG**GCGCCTAGTG TAGCCATCGAGGGACTTGACTTGTGTGTTTTCTGAAGTGTTCGAGGGTACCAGGAGAGCTG GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT CCTCTGACAAGTTACCTCACCTAATTTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCACTATATTCTAAGCACTTACAT GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTTACTTGTCCTGTCAC TGGATCTGGGCTAAAGTCCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAAACATGAATAAAACACATTTTATTCT AAAA



MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDWTEAVNF
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEÄLAFKWPF
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Signal sequence: amino acids 1-18

N-glycosylation site: amino acids 158-162

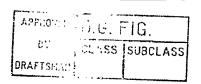
cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 76-80

Casein kinase II phosphorylation site: amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

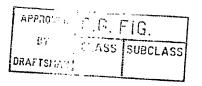
N-myristoylation site: amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site: amino acids 74-78

TGF-beta family signature: amino acids 282-298



GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCG**ATG**GGGACAAA GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG CATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTGGGAACCGGG CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT GTGGAGCGGAATGTGGGGGTCATCGTGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAAT CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG ACCTCGTCATTCCTGGTG**TGA**GCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT CAGGTGCTACCGGACTCTGGCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC TACACCCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC ATCCTCCTTCATGCCCTCCCTCCCTTTCCTACCACTGCTGAGTGGCCTGGAACTTGTTTAAA GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC TTCTAAGTAGACAGCAAAAATGGCGGGGGTCGCAGGAATCTGCACTCAACTGCCCACCTGGC TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGAC GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACTGGAGGCTGGGCGCAGTGGCTCACGCCTG TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTCGGGATCAGCCTGACCA ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC



MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
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SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
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Signal sequence: amino acids 1-27

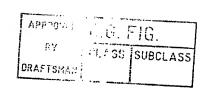
Transmembrane domain: amino acids 238-255

N-glycosylation site: amino acids 185-189

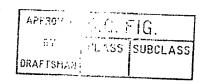
cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 270-274

Casein kinase II phosphorylation site: amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158, 193-197, 203-207, 287-291

N-myristoylation site: amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262



CAGCGCGTGGCCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA GCGTGGCGAACAGGGGCTCTGGGCCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT GGAGGCCGCGGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGCAGGCCCGAGCTCAG GCTCGTGCCCACCAAGTTCCAGTGCCGCACCAGTGGCTTATGCGTGCCCCTCACCTGG CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC ATGTACCCAGAAAGGGCAATGCCCACCGCCCCTGGCCTCCCCTGCCCCTGCACCGGCGTCA GTGACTGCTCTGGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCCTGGCCTAGCA GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCACCTCTCTCAGGAATGCC ACAACCATGGGGCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTCGGGAATGCCACATCCTC CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC TCAGTGCAAGCCTGGTCACCGCCACCCTCCTTTTTGTCCTGGCTCCGAGCCCAGGAGCGC CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGAC CTCGCTGCCC**TGA**GGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT CTGGCCACGTGGAACCTCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG GGGCTGGCCCAGGCAGCTCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC



MSGGWMAQVGAWRTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASEVTATLL
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Signal sequence: amino acids 1-30

Transmembrane domain: amino acids 230-246

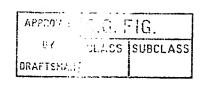
N-glycosylation site: amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site: amino acids 84-88, 140-144, 161-165, 218-222

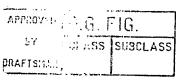
N-myristoylation site: amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218, 224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 44-55

Leucine zipper pattern: amino acids 17-39



CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGCAGCAGAGGTCGCGCACAGATGCGG CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAGCACCTCAGTCCCCCCAGAGACTCTTG CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTCATGAAGGATTCAAGATCCGG TACCCCGACCTACACAATATGGTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCC CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTG CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCGTCT GCCACCCGCGCCTTGTGAGCGCTACAACCACGGAACTGTGGTGGAGTTTTACTGCGATCCT GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCTCCTGA CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTCGTCATC CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCCAGGGGGCCTCCCCGGAG TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG ACGAAGCTGTGAGTGCCTTGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG GGCTGCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA GTCTGTATTCACCTCCCAGGTGCCAAGAGAGCCCCCCCCTGCTTCGGACAACCCTGACATA GTTGTTCCTAAGAAAC**TGA**TTGATTAAAAAATTTCCCAAAGTGTCCTGAAGTGTCTCTTCAA ATACATGTTGATCTGTGGAGTTGATTCCTTTCCTTCTTGGTTTTAGACAAATGTAAACAA AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC CTGTTTCTTGACACAGACTGATTAAAAATTAAAAGNAAAAA



MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRELAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDFDFYVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHWVLFLRN

Signal sequence: amino acids 1-41

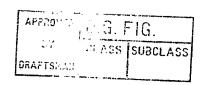
Transmembrane domain: amino acids 325-344

N-glycosylation site: amino acids 104-108, 134-138, 192-196

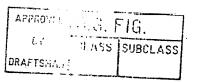
Casein kinase II phosphorylation site: amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366, 364-368, 380-384, 467-471, 468-472

N-myristoylation site: amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424, 478-484

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 394-405



CCCACGCGTCCGCTCCGCCCTCCCCCCGCTCCGTGCGGTCCGTCGGTGGCCTAGAGA TGCTGCTGCCGCGGTTGCAGTTGTCGCGCACGCCTCTGCCCGCCAGCCGCTCCACCGCCGT AGCGCCCGAGTGTCGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGACGGGTCGCCTGCTGAGTGCC TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCC GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT CACAATTTAGGAACTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTCATG TACCATCAGCCATCGGCACCGCTGGCATCGGAGGCCCCTACATGTTCCAGTGGAATGATGA CCGGTGCAACATGAAGAACAATTTCATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTT CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG GAAGAAGATGCCAAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT CCTAATCCCCAGCATTCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT GGATCTGTAGAAAAAGAAAACGGGAGCCAGACCCTAGCACAAAGAAGCAACACCCATC TGGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCATTCCGAGTGTGTT CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGA GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG GTTAT**TAG**GACATATAAAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTA GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG GCAGTGATAAAGATGGGCTGTGGAGCTTGGAAAACCACCTCTGTTTTCCTTGCTCTATACAG CAGCACATATTATCATACAGACAGAAAATCCAGAATCTTTTCAAAGCCCACATATGGTAGCA CAGGTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTTCAAAGAATAAAATCAAATAA AGAGCAGGAAAAAAAA



MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLV
VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence: amino acids 1-21

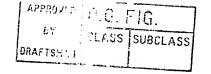
Transmembrane domain: amino acids 235-254

N-glycosylation site: amino acids 117-121, 312-316

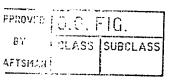
cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 296-300

Casein kinase II phosphorylation site: amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226, 299-303, 306-310, 323-327

N-myristoylation site: amino acids 18-24, 37-43, 76-82, 146-152



ATCCGCAGGTTCCCGCGGACTTGGGGGCCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCCAGCGAGGGCCTACCACCATGATCACTGGTGT AGCGGCGGTGGCCCTGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC $\tt CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC$ GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACTC AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTG CCACACTGATGAAGCAGATTCAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGA GGCAGAGACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT GGACAACGTGCCGAGCAGGCACACACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG CACGGATGATCGAACAGAGGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTTGACCACAAATGGCCACCGTTTGCT GTTGACCTGACCATGGAACTTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA ${\tt TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT}$ TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA ACTCAGGTGATGGAAGTTGGAAATGAAGAG**TAA**CTGATTTATAAAAGCAGGATGTGTTGATT TTAAAATAAAGTGCCTTTATACAATG



MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHIESKEW FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVYTLSPEKYHALCSQTQVMEVGNEE

Signal sequence: amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 218-222

Casein kinase II phosphorylation site: amino acids 87-91, 104-108, 320-324

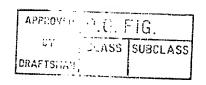
Tyrosine kinase phosphorylation site: amino acids 280-288

N-myristoylation site: amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

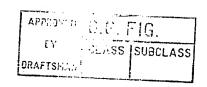
Amidation site: amino acids 216-220

Leucine zipper pattern: amino acids 10-32

Histidine acid phosphatases phosphohistidine signature: amino acids 50-65



CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT TAAATTTCAGCTCATCACCTTCACCTGCCTTGGTCATGCTCTGCTATTCTCCTTGATCCTT GCCATTTGCACCAGACCTGGATTCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGĠĠGGCCT CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG ACGGCTGGGACATTAAGGACGTGGCTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAGAGCAAAAGGTCCTCATĆĈA ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG ATTGTTCACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA GTCCCAGAGGGTGTCAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCG AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTCGTTGCTCAGGGGAGGAG TGTGGCTGTCATCTGCTCAGTG**TAG**GTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCCTGATTCTCAGGCCTTCAGAGTTGG ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG TATGTGTTCAAA



MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
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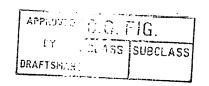
Signal sequence: amino acids 1-15

Casein kinase II phosphorylation site: amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238, 267-271, 294-298, 316-320, 336-340

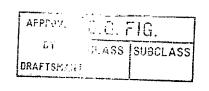
N-myristoylation site: amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143, 180-186, 263-269, 286-292

Amidation site: amino acids 196-200

Speract receptor repeated domain signature: amino acids 29-67, 249-287



ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC CCACGCGTCCGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCTGCTGTTCGGCTGCCTGGG CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGAAGGCCTACCTGCGGAATGCTG TGGTGGTGATCACAGGCCCCCCCCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTĆTATGC GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA TGTGGACAAGAGGGTCATGGAGACAAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC TGCCCTCCATGATCAAGAGGAGGCCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA ${\tt TCCACACCTACTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC}$ ACCACCACAGGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC $\verb|AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC|\\$ TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTA С



MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKĖŘKSKNS

Signal sequence: amino acids 1-21

Transmembrane domain: amino acids 104-120, 278-292

N-glycosylation site: amino acids 228-232

Glycosaminoglycan attachment site: amino acids 47-51

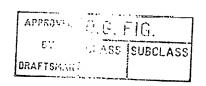
Casein kinase II phosphorylation site: amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site: amino acids 145-153, 146-153

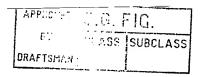
N-myristoylation site: amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site: amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 6-17



CCCACGCGTCCGCTGTTTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA AAAAAAAAAACACCAAAACGCTCGCAGCCACAAAAGGGG ATG AAATTTCTTCTGGACATCCTCCTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCCTAA GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATĀAG CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATÁCCTTTGT GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA GGCATTTCTTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG TTTCATAAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG TCTGTGTCCTAATTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA CCTGGCAGTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA AAGCGCAA**TAA**GCACCTAGTTTTCTGAAAACTGATTTACCAGGTTTAGGTTGATGTCATCTA ATAGTGCCAGAATTTTAATGTTTGAACTTCTGTTTTTTTCTAATTATCCCCATTTCTTCAATA TCATTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT CCAAAATGACTTTATTAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACTCTCAATGGGTAGGTTTC ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG



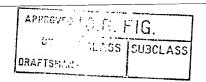
MKFLLDILLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
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YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
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Signal sequence: amino acids 1-19

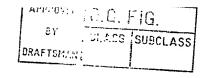
cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 30-34, 283-287

Casein kinase II phosphorylation site: amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site: amino acids 43-49, 72-78, 122-128, 210-216



TTTCGCTGGTCCTGTTGATGCCTGGCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC TGGGAAGATCCAAAAAGGAAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTĞAACATGA AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC TTCCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG AGGTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGA CCTTGCGTGACAGAGTTCCCCTGGACCACACGCTCTCCATGCTTTACATTGACAATCCA GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT AGCACGGGATTTATACAGTGCACTAATTCAGTTTTTCCAGATATTTCCTGAATATAAAAATA ATCCATTCCCTCAACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC AGGAAGCAGAACTGGTTTGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAA GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACTATAGTTGAAAAGTACTTGCGAGA AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA $\verb|TTCATTTATGGAAAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAAAGAGAACAT|$ CAGAGGTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAA TTATCTTTTCATATCTGCAAGATTTTTTTCATCAATAAAAATTATCCTTGAAACAAGTGAGC TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA AATTTTAGGGTCTTGAATAGGAAGTTTTAATTTCTTCTAAGAGTAAGTGAAAAGTGCAGTTG TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA AAAATATTATATATAAAAGTAAAAAAAAA



MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGRELSL
VGPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGSSMFGLFVEH
GPYVVTSNMTLRDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSÄLIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDRESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence: amino acids 1-22

N-glycosylation site: amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site: amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352, 353-357, 424-428

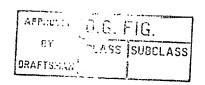
Tyrosine kinase phosphorylation site: amino acids 423-432

N-myristoylation site: amino acids 22-28, 110-116, 156-162, 232-238

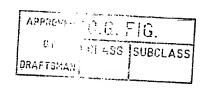
Serine carboxypeptidases, serine active site: amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature: amino acids 375-391





CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT TTTTCCCTTTCCTAACAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC CTGGGGGAGGCCTGCCTAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT TGAACTTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA GACCAAAATAGATAACAGGATTCCCTGAACATTCCTAAGAGGGAGAAAGTATGTTAAAAATA GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGG**ATG**GGGACCCTGGGTC AGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTTGGTCTGACCACTCTGCCTTGTGTTTT CCTCACCGCCCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG ACAGCCGCTCTGTGGTCCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCAGCAGCCGGC ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT CCACCAAGGGACGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG CCCCTCATCGTGCAGCCCTGCAGCGAAGTGCTCACCCTCACCAACAATGTCAACAAGCTGCT CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCA GCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT TTTGTCTCCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT CTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTTCGGCTGCACCCGGGC CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG CAGTATCACCACCCGCCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTT GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC TGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA CTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC CAGCAGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC ATTCACCTCCTCAGCAAAGAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG GCAACTTTATTTCTTGGGGAACAAAGG TGA AATTGGGGAGGTAAGAAGGGGTTAATTTTGTGACTTAGCTTCTAGCTACTTCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA TTTCAATATTTCCCAAACTTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA



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YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLACGSL
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence: amino acids 1-32

Transmembrane domain: amino acids 71-87

N-glycosylation site: amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site: amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387, 384-388, 471-475, 481-485, 530-534

N-myristoylation site: amino acids 220-226, 319-325, 353-359, 460-466, 503-509

64/133

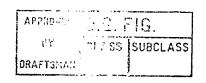


FIGURE 63A

AGGCTCCCGCGCGCGGTGAGTGCGGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAA CACGCGATGACCACGTGGAGCCTCCGGCGGAGGCCGGCCCGCACGCTGGGACTCCTGCTGCT GGTCGTCTTGGGCTTCCTGGTGCTCCGCAGGCTGGACTGGAGCACCCTGGTCCCTCTGGGGC TTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCCAGGGAGTACTGGAGGGACCG CCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCCTCACCACCTATGTTCCGTGGAACCTGC ATGAGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTGCTC ATGGCCGCAGAGATCGGGCTGTGGGTGATTCTGCGTCCAGGCCCCTACATCTGCAGTGAGAT GGACCTCGGGGGCTTGCCCAGCTGGCTACTCCAAGACCCTGGCATGAGGCTGAGGACAACTT ACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCACCTGATGTCCAGGGTGGTGCCA TAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGG AACTGCTCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTG GCCACCATCAACTTGCAGTCAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGT CCAGGGGACTCAGCCCAAGATGGTGATGGAGTACTGGACGGGGTGGTTTGACTCGTGGGGAG GCCCTCACAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGTCTGCCATTGTGGACGCC GGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATGGAGC CATGCACTTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAG AAGCCGGCGATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGC ATCCCTCTCCCTCCCCACCTGACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGT CTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACCTGGGGGAGCCAATCAAGTCTGAAAAGC CCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCCTTCGGGTACATTCTC TATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGGT GTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCC TGATCCAGGGTTACACCGTGCTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGG GAGAATATTGATGACCAGCGCAAAGGCTTAATTGGAAATCTCTATCTGAATGATTCACCCCT GAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGAGCTTCTTTCAGAGGTTCGGCCTGG ACAAATGGNGTTCCCTCCCAGAAACACCCACATTACCTGCTTTCTTCTTGGGTAGCTTGTCC ATCAGCTCCACGCCTTGTGACACCTTTCTGAAGCTGGAGGGGCTGGGAGAAGGGGGTTGTATT CATCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCCAGAAGACGCTTTACCTCC

To Figure 63B

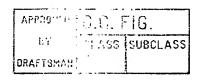
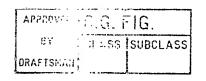


FIGURE 63B

From 63A

CAGGTCCCTGGTTGAGCAGCGGAATCAACCAGGTCATCGTTTTTGAGGAGACGATGGCGGGC CCTGCATTACAGTTCACGGAAACCCCCCACCTGGGCAGGAACCAGTACATTAAG**TGA**GCGGT GGCACCCCTCTGCTGGTGCCAGTGGGAGACTGCCGCCTCCTCTTGACCTGAAGCCTGGTG GCTGCTGCCCCACCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGGAĆTGGGGG CTACAGTCTGCCCCTGTCTCAGCTCAAAACCCTAAGCCTGCAGGGAAAGGTGGGÄTGGCTCT GGGCCTGGCTTTGTTGATGATGGCTTTCCTACAGCCCTGCTCTTGTGCCGAGGCTGTCGGG TGTCTCTAGGGTGGGAGCAGCTAATCAGATCGCCCAGCCTTTGGCCCTCAGAAAAAGTGCTG AAACGTGCCCTTGCACCGGACGTCACAGCCCTGCGAGCATCTGCTGGACTCAGGCGTGCTCT TTGCTGGTTCCTGGGAGGCTTGGCCACATCCCTCATGGCCCCATTTTATCCCCGAAATCCTG GGTGTCACCAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTTCTTCC TTCCCCTTTCCCTTCCCACTCGCTGCTTCCCACAGGGTGACAGGCTGGGCTGGAGAAACAGA AATCCTCACCCTGCGTCTTCCCAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATG TGAGTCCTGGCAGAAGCCATGCCCATGTCTGCACATCCAGGGAGGAGGACAGAAGGCCCAG CTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGGACAGA AGGCCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGG AGGACAGAAGGCCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATC CAGGGAGGAGGACAGAGGCCCAGCTCAGTGGCCCCGCTCCCCACCCCCCACGCCCGAACA GCAGGGGCAGAGCCCTCCTTCGAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTTCTGGG GCCCAGCCCAACACCTGGCTTGGGCTCACTGTCCTGAGTTGCAGTAAAGCTATAACCTTGAA **TCACAA**

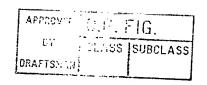


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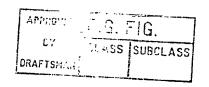
Signal sequence: amino acids 1-27

Casein kinase II phosphorylation site: amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site: amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315, 320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586



GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC ${\tt CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC}$ AAGAAGCTGTCCTGCCTTCCTTCCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCA GGCAGACACTCGGTCGTTCGTAGTGGATAGGGGTCATGACCGGTTTCTCCTAGACGGGGCCC CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGAC. CGGCTTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACTA CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGA ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG TGGGAGATGGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC AGATCCAGACTTCCTTGCCGCAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCGTGCACTGCTAGG GACTCTATACCACTGTAGATTTTGGCCCAGCTGACAACATGACCAAAATCTTTACCCTGCTT CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC TATATCTGAAGCAGGGGACCCCACACCTAAGCTTTTTGCTCTTCGAGATGTCATCAGCAAGT TCCAGGAAGTTCCTTTGGGACCTTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCAT TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC GAACCTATATGACCCATACCATTTTTGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC CATGACCGTGCCTATGTGATGGTGGATGGGGTGTTCCAGGGTGTTGTGGAGCGAAATATGAG AGACAAACTATTTTTGACGGGGAAACTGGGTCCAAACTGGATATCTTGGTGGAGAACATGG GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG GTGGTTTCCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC ACAACAGACCCTCTACGTGCCAAGATTCCTGCTGTTTCCTAGGGGAGCCCTCAACAAAATTA CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTTGGATAAGCCTATC CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCCTTTCAGCTGATACACTGAG TGCCTCTGAACCAATGGAGTTAAGTGGGCAC**TGA**AAGGTAGGCCGGGCATGGTGGCTCATGC CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA CCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTAAAAATACAAAAATTAGCCGGGCGTG ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA GACACTCCATCTCAAAAAAAAAAAA



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Signal sequence: amino acids 1-27

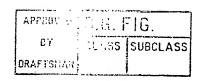
N-glycosylation site: amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 4-8

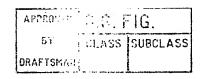
Casein kinase II phosphorylation site: amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554, 603-607, 644-648

Tyrosine kinase phosphorylation site: amino acids 191-198

N-myristoylation site: amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233, 231-237, 274-280, 296-300, 307-313, 447-453, 484-490



GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC ACCCACAAT**ATG**GCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTCAGGATACCTTTGAAGGAATATT CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT GCGTTCCTTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTTGGTGTGTT CTTGTCAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTĞGA&ATTTG AAAAACTCAGGCAGCACATTTCACGCAACGCCCAGGACAAGCAGGAGTTGCAŤĊTGTTCATG CTGTCGGGGGTGCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGĆT#GAACT AATTCCAGAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACTCCAGA ACTGTGAGCTAGAGAGAATCCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT AAAACTTGGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT AGTTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAGTGGACATTCTGC CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC CTTGGACCGCCTGCCAGCCCAGCTGGGCCAGTGTCGGATGCTCAAGAAAAGCGGGCTTGTTG TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA AATATTCCCTTTGCAAATGGGATT**TAA**ACTAAGATAATATATGCACAGTGATGTGCAGGAAC AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG ATACATCTTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT TTCTTACTAAAAAAAAAAAAAAAAAA



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Signal sequence: amino acids 1-20

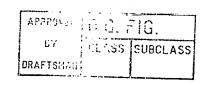
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cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 326-330

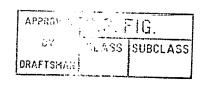
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Tyrosine kinase phosphorylation site: amino acids 349-355, 375-381

N-myristoylation site: amino acids 78-84, 124-130, 212-218, 392-398



CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCCTTTTCATTGACAAACTGAC TTTTTTTTTTTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGA CATTTGTGTTTTACACACATAAGGATCTGTGTTTTGGGGTTTCTTCTTCCTCCCCTGACATTG CTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTCATCGCTGGTG GTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCGTGCTCTGTCTTTACTTCAAAATACAC AACGCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAA GGTGTGGTGGCCAAGAACAGCCAGGCCAAAACCATTGCCACGGAGTCTTGTCCTGCCCTGC AGTGCTGTGAAGGATATAGAATGTGTGCCAGTTTTGATTCCCTGCCACCTTGCTGTTGCGAC ATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAAAGCAGAGCCCTGAAGACTTCA ATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAGCTCCCCA TCAGTTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAG AATGCTGATAAACCAGTCACACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCT GGAACTGACGTTTCCCTGGAGGTGTCCAGAAAGCTGATGTAACACAGAGCCTATAAAAGCTG TCGGTCCTTAAGGCTGCCCAGCGCCTTGCCAAAATGGAGCTTGTAAGAAGGCTCATGCCATT GACCCTCTTAATTCTCTCCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAATGCAA GCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAA CTCAATCCCAGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAAGCATCAGAAT TATCTTTTCCTATGTCCAGCTTGATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCT TTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGGCAAGTCTGCAGTAAAAACGACTATGTT CCTGTATTTGAATCATCCAGTACATTGACGTTTCAAATAGTTACTGACTCAGCAAGAAT TCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCTAACATCTCTATTCCAAACTGTG GCGGTTACCTGGATACCTTGGAAGGATCCTTCACCAGCCCCAATTACCCAAAGCCGCATCCT GAGCTGGCTTATTGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAAACTT CAAAGAGATTTTCCTAGAAATAGACAAACAGTGCAAATTTGATTTTCTTGCCATCTATGATG GCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGTGGCCGTGTGACTCCCACCTTCGAA TCGTCATCAAACTCTCTGACTGTCGTGTTGTCTACAGATTATGCCAATTCTTACCGGGGATT TTCTGCTTCCTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTT CTGACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAAT AACTTGCAACTAAAAGACCCAACTTGCAGACCAAAATTATCAAATGTTGTGGAATTTTCTGT TAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACCCGTCAGAAACAACTCCAGATT ATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACAGAAGATGA TGTAATACAAAGTCAAAATGCACTGGGCAAATATAACACCAGCATGGCTCTTTTTGAATCCA ATTCATTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACTCTTTTT GTTCAAGTTAGTCTGCACACCTCAGATCCAAATTTGGTGGTGTTTTCTTGATACCTGTAGAGC CTCTCCCACCTCTGACTTTGCATCTCCAACCTACGACCTAATCAAGAGTGGATGTAGTCGAG ATGAAACTTGTAAGGTGTATCCCTTATTTGGACACTATGGGAGATTCCAGTTTAATGCCTTT AAATTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAAGTTTTGATATGTGATAGCAG TGACCACCAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCAT ATAAATGGAAAACAGATTCCATCATAGGACCCATTCGTCTGAAAAGGGATCGAAGTGCAAGT GGCAATTCAGGATTTCAGCATGAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAG TGTGCATCTGTTTTCCTTCATGGTTCTAGCTCTGAATGTGGTGACTGTAGCGACAATCACAG TGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTGCAGAACTAT**TAA**CTA ACAGGTCCAACCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGTGG CTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAA AAA



MELVRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGQVCSKNDYVPVFESSSTLT
FQIVTDSARIQRTVFVFYYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYÇVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDSIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence: amino acids 1-24

Transmembrane domain: amino acids 571-586

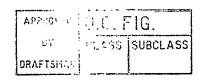
N-glycosylation site: amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374, 394-398, 419-423

Casein kinase II phosphorylation site: amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383, 408-412, 463-467, 520-524, 556-560

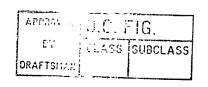
Tyrosine kinase phosphorylation site: amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site: amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 7-18



GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGACAGCCGGCCTGCGCCG GGACATGCGGCCCCAGGAGCTCCCCAGGCTCCCGTTGCTGCTGTTGCTGTTGCTGC TGCTGCCGCCGCCGTGCCCTGCCCACAGCGCCACGCGCTTCGACCCCACCTGGGAGTCC CTGGACGCCCGCCGCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTGATCCACTG GGGAGTGTTTTCCGTGCCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACCAGTGGGCAGATATTTTTCAGGC CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT CAGAATATTCGTGGAACTGGAATGCCATAGATGAGGGGCCCCAAGAGGGACATTGTCAAGGAA CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTTGGACTGTACTATTCCCTTTTTGA ATGGTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG TCGGATGGTGACGGAGGACCCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT ATATAATGAAAGCCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA CATAAATGGGAAAACTGCATGACAATAGACAAACTGTCCTGGGGCTATAGGAGGGAAGCTGG AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG GAGGAAATCTTTTGATGAATATTGGGCCCACACTAGATGGCACCATTTCTGTAGTTTTTGAG GAGCGACTGAGGCAAGTGGGGTCCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA TACCTGGCGATCCCAGAATGACACTGTCACCCCAGATGTGTGGTACACATCCAAGCCTAAAG AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCCACATCAGGACAGCTGTTCCTTGGCCAT CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG GATTTCTTTGGÄGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC CGTGTAAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATC**TAA**AGTGCAGCAGAGTGGCTG ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA AAGCAATGTAAACTGGATAAGAAAATTATTTGGCAGTTCAGCCCTTTTCCCTTTTTCCCACTA AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGCACTTTGCCATTAAAGTC TCTTCACATTGATTTCCATGTGTGACTCAGAGGTGAGAATTTTTTCACATTATAGTAG CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATG ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT TTTTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAĠ GTACAGTAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAATGTGAAGGCCTAGGACATTA GTTTTTCTTCAATTAAATTAACATAAGTGTACTGTAACTTTACAAACGTTTTAATT TTTAAAACCTTTTTGGCTCTTTTGTAATAACACTTAGCTTAAAACATAAACTCATTGTGCAA ATGTAA



MRPQELPRLAFPLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTĞFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHĞQPLNWÏ
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence: amino acids 1-28

N-glycosylation site: amino acids 171-175, 239-243, 377-381

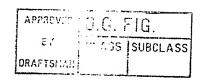
Casein kinase II phosphorylation site: amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319, 375-375

Tyrosine kinase phosphorylation site: amino acids 361-369, 389-397

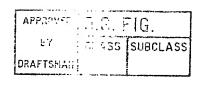
N-myristoylation site: amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern: amino acids 410-432

Alpha-L-fucosidase putative active site: amino acids 283-295



TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTTG CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGC AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGA... TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGAT ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA AACTGCAACACAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT ACTCTACAATACCTGCCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG AGAAAAAATTGATTTGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAAC TGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAA TTACCCTGCCCCAGCTGGGGAAATCAAAAGGGCCCAAAGAACCAAAGAAGAAGTCCACCCTT GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC TTTCTAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAA GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG TGGGTTGAAAGCCAAGGATCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGAC CCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTA AGAGCAAAAGATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTTATCTGA GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT TGAATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCA ATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG TACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAACAAATGTATCACTA GCCCTCCTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA AGCATTTAGAAAACTT



MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence: amino acids 1-16

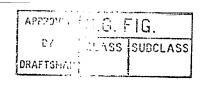
Transmembrane domain: amino acids 235-254

N-glycosylation site: amino acids 53-57, 130-134, 289-293

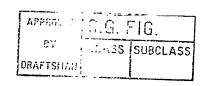
Casein kinase II phosphorylation site: amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site: amino acids 79-88

N-myristoylation site: amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259



AGATGCCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTCGGTGCCGCGACTTTCACGATGG CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAA ACTGCCGCCGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG ACTGGAGAGAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACGGCAGA TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAÄCACAAT TCTTTCTTCCGCTTGGATATTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTCC TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAÄ ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA TTGGTCTAATGACTGCCAATCATTTGCCCCTATCTATGCTGACCTCTCCCTTAAATACAACT GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTCAGA TGGGGAAAACAAGAAGATAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATT CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAACTGTTTCACTGGAGCAAGAAGAGATC TCATAGGACGGAGGGGAAATGGTTTCCCTCCAAGCTTGGGTCAGTGTGTTAACTGCTTATC AGCTATTCAGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCCTTCTTAG TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAA CGCTAAGAATTTTCCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC TTCATTAAAAGTATAAGCCTAACTTTGTCGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG TTTTTATCATTGAAGACAATATTGAACAACCCCCTATTTTGTGGGGATTGAGAAGGGGTGAA TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCAC TAACCCTCTGACATACTCCCCACACCCAGTTGATGGCTTTCCGTAATAAAAAGATTGGGATT TCCTTTTG



MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence: amino acids 1-48

Transmembrane domain: amino acids 111-125

N-glycosylation site: amino acids 165-169, 185-189

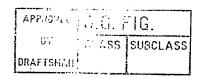
cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 154-158, 265-269

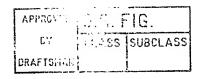
Casein kinase II phosphorylation site: amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site: amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1: amino acids 244-253



GGACAGCTCGCGGCCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTG GGGCCCCAGCCTGGCCCGGGTCACCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCCA TTGCTCCTGCTGCCCGGCTCCTACGGACTGCCCTTCTACAACGGCTTCTACTACTACTCCAACAG CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG TGGTGGAGACACCCGAGGAGACCCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGGAAGCT GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT... TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCATTGACGGGCTGGA GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGTCTTTCCTTACCAGTCCCCA ACGGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG GTGGCCTCCTTTGAGCAGCTCTTCCGGGCCTGGGAGGGGCCTGGACTGGTGCAACGCGGG $\tt CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCCGGCAGCCCTGCGGTGGCC$ CAGGCCTGGCACCTGCGTGCGAAGCTACGGCCCCCGCCACCGCCGCCTGCACCGCTATGAT GTATTCTGCTTCGCTACTGCCCTCAAGGGGCGGGTGTACTACCTGGAGCACCCTGAGAAGCT GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGGAC GGCAGCGTCCGCTACCTGTGGTTCACCCGCATCCTAACTGTGGGCCCCCAGAGCCTGGGGT CCGAAGCTTTGGCTTCCCCGACCCGCAGAGCCGCTTGTACGGTGTTTACTGCTACCGCCAGC CGTTTTCCCTTGTGGGTTGGAGCCATTTTAACTGTTTTTATACTTCTCAATTTAAATTTTCT TTAAACATTTTTTACTATTTTTTGTAAAGCAAACAGAACCCAATGCCTCCCTTTGCTCCTG GATGCCCCACTCCAGGAATCATGCTTGCTCCCCTGGGCCATTTGCGGTTTTGTGGGCTTCTG GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCCAGAGTGGGC GGTGGCCTGTCTAGAATGCCGCCGGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCCT CAGCCTGGGGGAAGAAGAGGGCCTCGGGGGCCTCCGGAGCTGGGCTTTGGGCCTCTCCTGCC CACCTCTACTTCTCTGTGAAGCCGCTGACCCCAGTCTGCCCACTGAGGGGCTAGGGCTGGAA TCCCCTCTCGGTTCCAAAGAATCTGTTTTGTTGTCATTTGTTTCTCCTGTTTCCCTGTGTGG GGAGGGCCCTCAGGTGTGTACTTTGGACAATAAATGGTGCTATGACTGCCTTCCGCCAA



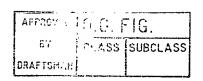
MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence: amino acids 1-17

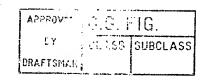
Casein kinase II phosphorylation site: amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site: amino acids 137-145

N-myristoylation site: amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313



GGAGAGCGGAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC TTCTGTTGCTACTGAGGCACGGGGCCCAGGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC CAGGGGAGGGTGCACCAGGCGCCCCCTGAGCGACGCTCCCCATGATGACGCCCACGGGAA CTTCCAGTACGACCATGAGGCTTTCCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTGA CCCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGGGGGGAC GGCGACGCTGGGTGTCGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGCAC CATACGGGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGGACCGCGACGGGGTGTGG GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTCATGAC GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGC CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGG AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCCTGGAGGACCTGGACAGAAACAAA GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA GGAGCCGGCGTGGGTGCAGACGGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGG ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCTGCCCAGGACCAGCCC CTGGTGGAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG ACCTGACCCGGCACCACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG GCAGATGCAGTCCCAGGCATCCTCCTGCCCCTGGGCTCTCAGGGACCCCCTGGGTCGGCTTC TGTCCCTGTCACACCCCCAACCCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC CTATTTCTGACTGAGTCTCCCAGCCCAGACCCAGGGACCCTTGGCCCCAAGCTCAGCTCTAA GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCT GGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA AAAAAAAAAAAA



MMWRPSVLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT YDTDRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ FRDFRDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV GSQATNYGEDLTRHHDEL

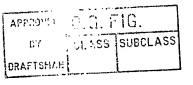
Signal sequence: amino acids 1-20

N-glycosylation site: amino acids 140-144

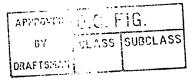
Casein kinase II phosphorylation site: amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293, 291-295, 298-302

N-myristoylation site: amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence: amino acids 325-330



GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG GCGCGGGCGCGGGTGCGAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTCGCTCCCAG CCTGTCTGTCGTCGTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTTGCACACCGATCCTG 🔩 GGCTTCGCTCGATTTGCCGCCGAGGCGCCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG CGGGTCGTCTGTGCCTCTCCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCGGGGCTCT GAGGAGGTGACGCGCGGGCCTCCCGCACCCTGGCCTTGCCCGCATTCTCCCTCTCTCCCAG GTGTGAGCAGCCTATCAGTCACC**ATG**TCCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG TGTCTGCTGCTGCCGGGGCCCGCGGGCAGCGAGGCGCTCCCATTGCTATCACATG TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCCAGGGGGCTGCC CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC TGGTCGAGAAAACTATTCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT GGTCTGCTTCTTTCACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACTGG GCCGATTTAATTTACAGAAGAATTTTGTTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA GAAGGACCACATGTGGGCCTTGTTCAAGCCAGTGAACATCCCAAAATAGAATTTTACTTGAA AAACTTTACATCAGCCAAAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCTGGA GTAAGAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT CGAGGAAGCAGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTTGGAGATAGCAATTTCCGCCTC ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGAT AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACCA AAGAGAATGTCCTAGCTGTCATCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT GATGCCATTTCCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAGAA CTTCCTAGTAATTGTCACAGATGGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCCTTGGGCACCTCTGGATGACCTG AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCACAAGAGAGTTCACAGGATT AGAACCAATTGTTTCTGATGTCATCAGAGGCATTTGTAGAGATTTCTTAGAATCCCAGCAAT **AA**TGGTAACATTTTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGTATT CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAACTATTAAGTATGTCAAC AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA



MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIÄFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAĠĬTI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQO

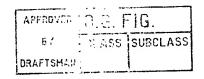
Signal sequence: amino acids 1-24

N-glycosylation site: amino acids 100-104, 221-225

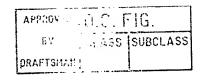
Casein kinase II phosphorylation site: amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424, 425-429, 478-482, 528-532

N-myristoylation site: amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211, 239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site: amino acids 145-149



CGCCGCGCTCCCGCACCCGCGCCCCACCGCGCCCCCCCATCTGCACCCGCAGCCC GGCGGCCTCCCGGCGGAGCGAGCCAGTCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG TGCTGGCGGCGGCCCCACGGCCCCGCGCCCGCTCCGACGCCGACCTCGGCTCCAGTC AAGCCCGGCCCGGCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA GGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG CAGAAGAAGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACTTACCTCCCAGCTAT TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG TGGGAGACGAAGAAGGCAGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCCAGC CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGGTCACTGCACCAAAA TGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTG TGCTGTGCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGGAGCCTGCGGCTGCCGCCT GCACTGCTGGGAGGGGAAGAGATT**TAG**ATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTACA TCTTCTTCCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTCAGC TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAG ACAGCCGTTTGTTCTACATGGCTTTGATAATTGTTTGAGGGGAGAGATGGAAACAATGTGG AGTCTCCCTCTGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAA CCTGGCAAAAATGCAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTG TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCCTGCATTACATGTGTTTATTCATCC AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC CCTCTCTCAGCACAGCCTGGGGAGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAG GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCCACACCAGCCTTGGTGCCACCAA AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTTCTTGAGGCATGCACATCTGGAATTAAG GTCAAACTAATTCTCACATCCCTCTAAAAGTAAACTACTGTTAGGAACAGCAGTGTTCTCAC AGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT TGCATTAGTAACTTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTCAGGTGTCA TGGACTGTTGCCACCATGTATTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA TAAGCATGCTTTCTTTGAGTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC



MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEEI

Signal sequence: amino acids 1-19

N-glycosylation site: amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site: amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316, 327-331

N-myristoylation site: amino acids 202-208, 217-223

Amidation site: amino acids 140-144

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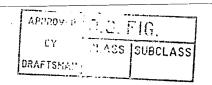


FIGURE 85A

CATGTGCATGTACACACACACACACACACACACACTCCTCCTCCTCCACTGAAGACTCA CAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGACAGGCCTGG CCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGGCCAGGCACGG TGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTCAG GAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCCATCTCTACTAAAAATACAAAAATT AGCCAGGAGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATC GCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCGCTGCACTCCAGCCTGGGT GCAACCTCCTTAACTCTGCATCCTCTTCTTCCAGGGCTGCCCCTGATGGGGCCTGGCAATGA CTGAGCAGGCCCAGAGCACAAGGAAGAAGGCATATTGAGGAGGCCAAGAAGTGA CGCCCGGTGTAGAATGACTGCCCTGGGAGGGTGGTTCCTTGGGCCCTGGCAGGGTTGCTGAC CCTTACCCTGCAAAACACAAAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCTGCCC TGCAGCTCCACC**ATG**AGGCTTCTCGTGGCCCCACTCTTGCTAGCTTGGGTGGCTGGTGCCAC GGCCCTGGTATACGCCCCGCTCGTCCTACCGCGAGGCTACCACTGTGGACTGCAATGACCTA TTCCTGACGGCAGTCCCCCGGCACTCCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAA CAGCATTGTCCGTGTGGACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACC TGTCCCAGAACAGCTTTTCGGATGCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTG AGCCTGCACCTAGAGGAGAACCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGC CAGCCTACAGGAACTCTATCTCAACCACAACCAGCTCTACCGCATCGCCCCCAGGGCCTTTT CTGGCCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGC CGCTGGTTTGAAATGCTGCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGC CATCCTGGACATGAACTTCCGGCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGA ACCTGCGGGAGATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTC TATGACAACCAGCTGGCCCGGGTGCCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAGTT CCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATGCTGC ACCTTAAGGAGCTGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTG GTGAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTCATCCA CCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCTCA

To Figure 85B

APPROVIDE TOLDS FIG.

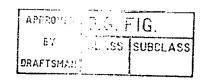
BY CLASS SUBCLASS

BRAFTSHAD

FIGURE 85B

From Figure 85A

AACCCCATCCGCTGTGACTGTCTCATCCGCTGGGCCAATGCCACGGGCACCCGTGTCCGCTT CATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCCGGTCCGTG AGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCCTCATCTCCCCACGAAĞCTTCCCC CCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGCACTGGCCGAACC CGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACCTGCCCATGCAGGCA GGAGGTACCGGGTGTACCCCGAGGGGACCCTGGAGCTGCGGAGGGTGACAGCAGAAGAGGCA GGGCTATACACCTGTGTGGCCCAGAACCTGGTGGGGGCTGACACTAAGACGGTTAGTGTGGT TGTGGGCCGTGCTCCTCCAGCCAGGCAGGGACGAAGGACAGGGGCTGGAGCTCCGGGTGC AACCTCACCTGGTCCAGTGCCTCCTCCCTCCGGGGCCCAGGGGGCCACAGCTCTGGCCCGCCT GCCTCGGGGAACCCACAGCTACAACATTACCCGCCTCCTTCAGGCCACGGAGTACTGGGCCT GCCTGCAAGTGGCCTTTGCTGATGCCCACACCCAGTTGGCTTGTGTATGGGCCAGGACCAAA GAGGCCACTTCTTGCCACAGAGCCTTAGGGGATCGTCCTGGGCTCATTGCCATCCTGGCTCT CGCTGTCCTTCTCCTGGCAGCTGGGCTAGCGGCCCACCTTGGCACAGGCCAACCCAGGAAGG GTGTGGGTGGGAGGCGCCTCTCCCTCCAGCCTGGGCTTTCTGGGGCCTGGAGTGCCCCTTCT GTCCGGGTTGTCTCCCCTCGTCCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATC CTCAGAAGGGGAGACACTGTTGCCACCATTGTCTCAAAATTCT**TGA**AGCTCAGCCTGTTCTC AGCAGTAGAGAAATCACTAGGACTACTTTTTACCAAAAGAGAAGCAGTCTGGGCCAGATGCC CTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGGCCAAGACAGATGG GGCTTTGTGGCCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTC ACCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCC GCCTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGGCTGCCCTCAATGT GGGAGTGACCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCCAGGAACGCCTCATC TCAGCAGCCTGGGCTCCGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGG AGAAATGTGTCACCTCCCCCAACCCGATTCACTCTTTTCTCCTGTTTTTGTAAAAAATAAAAA TAAATAATAACAATAAAAAAA



MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAEEAGLYT
CVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLLAAGLAAHLGTGQPRKGVGGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSONS

Signal sequence: amino acids 1-18

Transmembrane domain: amino acids 629-648

N-glycosylation site: amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 485-489

Casein kinase II phosphorylation site: amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146, 243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site: amino acids 532-540

N-myristoylation site: amino acids 15-21, 493-499, 566-572

Amidation site: amino acids 470-474, 660-664, 692-696

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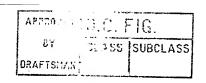


FIGURE 87A

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACA TTGTGTACCGCCTCTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATC TGCTACACCGTCTACTACGTGCACAACATCAAGTTCGACGTGGACTGCACCGTGGACATTGA GAGCCTGACGGGCTACCGCACCTGTGCCCACCCCTGGCCACACTCTTCAAGATCC TGGCGTCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTACACACTGTGG TGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGCAGCTA CAGCGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCÄÄTÄCG CAGCTGAACCTCAACAACGAGTGGACGCTGGACAAGCTCCGGCAGCGGCTCACCAAGAACGC GCAGGACAAGCTGGAGCTGCACCTGTTCATGCTCAGTGGCATCCCTGACACTGTGTTTGACC TGGTGGAGCTGGAGCTCCAAGCTGGAGCTGATCCCCGACGTGACCATCCCGCCCAGCATT GCCCAGCTCACGGGCCTCAAGGAGCTGTGGCTCTACCACACACGCGCCCAAGATTGAAGCGCC TGCGCTGGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGG AGATCCCGCTGTGGATCTATAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGCCAACCTG AGCGCGGAGAACAACCGCTACATCGTCATCGACGGGCTGCGGGAGCTCAAACGCCTCAAGGT GCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCACAGATGTGGGCGTGCACC TGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCCTCAACAGCCTCAAGAAG ATGGCGAACCTGACTGAGCTGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCAT CTTCAGCCTCCACAACCTGCAGGAGATTGACCTCAAGGACAACCTCAAGACCATCGAGG AGATCATCAGCTTCCAGCACCTGCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATC GCCTACATCCCCATCCAGATCGGCAACCTCACCAACCTGGAGCGCCTCTACCTGAACCGCAA CAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCGCTACCTGGACCTCA GCCACAACAACCTGACCTTCCTCCCTGCCGACATCGGCCTCCTGCAGAACCTCCAGAACCTA GCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCG GGCCCTGCACCTGGGCAACACGTGCTGCAGTCACTGCCCTCCAGGGTGGGCGAGCTGACCA TGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGAGGACCTGTTCAACACACTGCCACC ACAGCAAGCAGCAGGACCGCTGCCCAGTCCTCAGGCCCGGAGGGGCAGGCCTAGCTTCTCCC AGAACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCAGGAGCCTGGGGCCGCTTGTGAGT CAGGCCAGAGCGAGAGCACTATCTGTGGGGCTGGCCCCTTTTCTCCCTCTGAGACTCACG

To Figure 87B

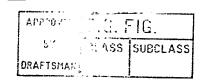


FIGURE 87B

From Figure 87A

TCCCCCAGGGCAAGTGCTTGTGGAGGAGAGCAAGTCTCAAGAGCGCAGTATTTGGATAATCA GGGTCTCCTCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAGCTGCCACCAGAGGTCCTGGGA CCCTCACTTTAGTTCTTGGTATTTATTTTTCTCCATCTCCCACCTCCTTCATCCAGATAACT TATACATTCCCAAGAAAGTTCAGCCCAGATGGAAGGTGTTCAGGGAAAGGTGGCCTTT* TGGTCCGGGGCGAACCAGCCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTG CGGTCCACGGGAGAGCAGGCCTCCAGCTGGAAAGGCCAGGCCTGGAGCTTGCCTCTTCAGTT ACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGTGGCAGTTTCCCTTGAGCAAAGCAG CCAGACGTTGAACTGTTTTCCTTTCCCTGGGCGCAGGGTGCAGGGTGTCTTCCGGATCTGG GGCTGTCGGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGAGGAGACTCGGGTTGGCTAA CACAGTGTTAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTCCCCACCTCCTGCGG CATGGGTGTCCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTCGCCACCTGG TCCTTCATGAAGAGCAGACACTTAGAGGCTGGTCGGGAATGGGGAGGTCGCCCCTGGGAGGG CAGGCGTTGGTTCCAAGCCGGTTCCCGTCCCTGGCGCCTGGAGTGCACACAGCCCAGTCGGC ACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTTAGAAGGGTCCCC GCCTTAGATCAATCACGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATG TCCATCCGTCTGTCCATTTGTGTTTTTCTGCGTCGTGTCATTGGATATAATCCTCAGAA ATAATGCACACTAGCCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACTT

ROYCO O.G. FIG.
BY CLASS SUBCLASS

FIGURE 88

MRQTIIKVIKFILIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEÈIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEOA

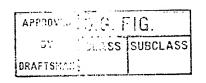
Transmembrane domain: amino acids 51-75 (type II)

N-glycosylation site: amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 85-89

Casein kinase II phosphorylation site: amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368, 398-402, 493-497

N-myristoylation site: amino acids 173-179, 261-267, 395-401, 441-447



 ${\tt GCCTGTTGCTGATGCTGCGGTGCGGTACTTGTC} \textbf{ATG} {\tt GAGCTGGCACTGCGGCGCTCTCCCGT}...$ CCCGCGTGGTTGCTGCTGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT GGCCCACAGAGGAGGCCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTÂCATG TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCAT GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAGGAAATTGGGC. CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT GTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG AATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC ATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT TGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTGCTCTCCTGGGGACCTTACCTGT ACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT GATCATTGAACAGAACACAGATGGGGTGAACTTCTATAACATCTTAACTAAAAGCACTCCCA CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCAGCGC GCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTG ACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTC TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT ${\tt GATGAGACTGGTGACTCAGCAAGAA} \textbf{TAG} {\tt GATGGGGGCTGGAGATGAGCTGGTTTGGCCT}$ TGGGGCACAGAGCTGAGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTTAAAAAATTGAT TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

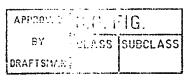


FIGURE 90.

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAFQR GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE ATELWGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL IVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP SDQGDMALKMMRLVTQQE

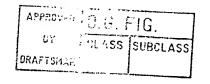
Signal sequence: amino acids 1-25

N-glycosylation site: amino acids 64-68, 126-130, 362-366

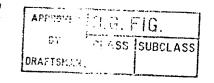
cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 101-105

Casein kinase II phosphorylation site: amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site: amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175, 187-193, 195-201, 331-337, 332-338, 360-366



GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGGCGCTGCTGCTGCTGCTGCTGCTC GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG CACTCACGGCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCTATGACATTG. CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAACA ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG GTTTGTGCTGCCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG GTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACTTTGAGTGGATCCAGAAG CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTCCCTCT CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGTTTTGGTAATAAACACATTCCAGTTGA



MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence: amino acids 1-18

N-glycosylation site: amino acids 167-171, 200-204, 273-277

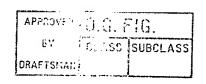
Casein kinase II phosphorylation site: amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site: amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245, 259-265, 269-275

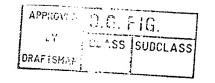
Amidation site: amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 252-263,

Serine proteases, trypsin family, histidine active site: amino acids 78-84



CTTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCGGAGCCCGACCAGCGGAGGACGC TGCCCCCAGGCTGGGTGTCCCTGGGCCGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCGGATĆĆCAG CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGĆCATCCC CACTGACCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCCAGAAGTGCCATTCT GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC. ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCCATGTGGACTTTGTGGGGGGGACTGCACCGT TTTCCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGCAGGTGACAGGGACTGTAGGCCT GCATCTGGGGGTAACCCCCTCTGTGATCCGTAAGCGATACAACTTGACCTCACAAGACGTGG GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCCAGTTCCTGGAGCAGTATTTCCATGAC TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT ACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTCAGTAATGAGTCAGCCCTGCCACATGT GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA ACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCCTGCTCTTCGCCTCAGGTGACAGT GGGGCCGGGTGTTGGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG CCCCTATGTCACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCCTCATCACAAATGAAA TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTTCATACCAGGAG GAAGCTGTAACGAAGTTCCTGAGCTCTAGCCCCCACCTGCCACCATCCAGTTACTTCAATGC CAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTTCTGATGGCTACTGGGTGGTCAGCAACA GAGTGCCCATTCCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTGTTTTGGGGGGGATCCTA TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAACCCAAG GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC $\tt TGGGGAACACCAACTTCCCAGCTTTGC \textbf{TGA} AGACTCTACTCAACCCCTGACCCTTTCCTATC$ AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCAGTCCCTTATTCTGCCCTGTTG GAAGCCCTGCTGAACCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCTGAAA TGCTGTGAGCTTGACTCCCAACCCTACCATGCTCCATCATACTCAGGTCTCCCTACT ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA TTTCACTTGATATTCATTCCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTTACTCT TTCCTACCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTTGCTTTATG GCCTTTCCATCATAGTTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACTTCTCTG ACTACTCTTGTCTTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGC TCCATTTGTAGATTTTTGCTCTTCTCAGTTTACTCATTGTCCCCTGGAACAAATCACTGACA **TGTAAAAA**



MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

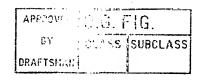
Signal sequence: amino acids 1-16

N-glycosylation site: amino acids 210-214, 222-226, 286-290, 313-317, 443-447

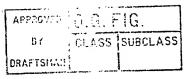
Glycosaminoglycan attachment site: amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site: amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site: amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225, 248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488, 521-527, 533-539, 549-555



GCCGCGCTCTCTCCCGGCGCCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC GGGCTGCTCGGCGCGAACAGTGCTCGGC**ATG**GCAGGGATTCCAGGGCTCCTCTTCCTTCTC TTCTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCCACTTG GCCTGCATACCGCCTCCCTGTCGTCTTGCCCCAGTCTACCCTCAATTTAGCCAAGCCAGACT TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGGACCCCAGTGTCATAAGGGAACT CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG CAGCCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC AGGTTCAGCATTTTTGGGAAGGACTTCCTGCTCAACTACCCTTTCTCAACATCAGTGAAGTT ATCCACGGGCTGCACCGGCACCCTGGTGGCAGAGAAGCATGTCCTCACAGCTGCCACTGCA TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCC AAGTTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCCGAGCAGATGAA ATTTCAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACTCAAAAAGCCCCACAAGAGAAAAA TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACTTCTC TGGTTATGACAATGACCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA CCTATGACTTGCTCTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGGTCTGGGGTCTAT GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTCAGG GCACCAGTGGGTGGACATGAATGGTTCCCCACAGGATTTCAACGTGGCTGTCAGAATCACTC **TGA**CACAGTGTTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTTTAGGAGAGGCC CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAACTG GTTTGTGTATCATATCATATCATTTAAGCAGTTTGAAGGCATACTTTTGCATAGAAATAA AAAAAATACTGATTTGGGGCAATGAGGAATATTTGACAATTAAGTTAATCTTCACGTTTTTG CAAACTTTGATTTTATTTCATCTGAACTTGTTTCAAAGATTTATATTAAATATTTGGCATA CAAGAGATATGAAAAAAAAAAAAAA



MAGIPGLLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYÄQICYW
IKGNYLDCREG

Signal sequence: amino acids 1-19

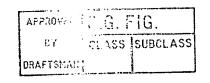
N-glycosylation site: amino acids 93-97, 207-211

Glycosaminoglycan attachment site: amino acids 109-113, 316-320

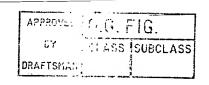
Casein kinase II phosphorylation site: amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site: amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site: amino acids 171-177



GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTCCCCCGCCCCACCAGCCATGGTGGTTT CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGGCCCA GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGÄTCGTGA GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC ACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGTGCTGCTGGG CCCACCTGTGTATTCCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG CGCTCCATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT CCCACCTCAGACCTGCAGAAGCTGAAGGTTCCTATCATCGACTCGGAAGTCTGCAGCCAT CTGTACTGGCGGGGAGCAGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT GGAGGGGGGCCCCTCATGTCCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG GCGCCTGGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA GCTCCGCGGGCGCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA TCTGGATCTGCGCCGCCGCCGTAAATAGGCTCATCTACC GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCCAACGGCCTCATGTCCCCGCCCCAC GACTTCCGGCCCCGGCCCCCGGGCCCCAGCGCTTTTGTGTATAAATGTTAATGATTTTTAT CTCCAAAAAAAAAA



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><subunit 1 of 1, 317 aa, 1 stop

><MW: 33732, pI: 7.90, NX(S/T): 1

MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSOKVGVA WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG SGAAARS

Signal sequence: amino acids 1-32

N-glycosylation site: amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459, 628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site: amino acids 826-830

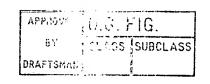
Casein kinase II phosphorylation site: amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268, 314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653, 671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962, 1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site: amino acids 607-615

N-myristoylation site: amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534, 612-618, 623-629, 714-720, 873-879



GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC AACAAGGAGCGCGGCGCGGCGAGAATCTGTTCGCCATCACAGACGAGGGCATGGACGT GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGÄGGATC GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTTGAGGAGACCAACATCGAATTACT GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGGAAACGGCCCTACCAGGAGGGGACTC CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGA AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGTGGAAACCCAGGCC CCAACTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA AAAGTGCCCTCTAGGAGCCCAGAGACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG GGAACTCCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTCCCCCAATACCTCTGCCACCGCTAA TGCCACGGGTGGGCTGCCCTGGCTCTGCCAGTCCTTGCCAGGTGCAGAGGGCCCTGACA AGCCTAGCGTTGTGTCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA $\tt CTACTGCTCCTCCTCTGGTGTTTGGCTGGAATCTTC\textbf{TGA} ATGGGATACCACTCAAAGGG$ TGAAGAGGTCAGCTGTCCTCCTGTCATCTTCCCCACCCTGTCCCCAGCCCCTAAACAAGATA CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACC CACTGCCTACCTGGCCTGGGGCTGTCTGCCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG TGTAGCTGGGGATGGGGATTCCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC TTTGAGTGGGGGAGGCAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCT GTCCAACCTGTGAAA



MHGSCSFLMLLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEAELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPPLVLAGIF

Signal sequence: amino acids 1-22

N-glycosylation site: amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site: amino acids 439-443

Casein kinase II phosphorylation site: amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site: amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

Amidation site: amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature: amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1: amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2: amino acids 160-172

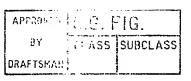


FIGURE 101A

GTAACTGAAGTCAGGCTTTTCATTTGGGAAGCCCCCTCAACAGAATTCGGTCATTCTCCAAG TTATGGTGGACGTACTTCTGTTGTTCTCCCTCTGCTTTTTTCACATTAGCAGACCGGAC TTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTTCG AGAAGTGAAACTGAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGTCTCGGCAA ATATTACACTTCTCTCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAA GAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTCAGAGCTCCAAAGTGC ATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAAC CTGGGTATTTTGACAATTTGGCCAACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATC TCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAACATCTCGAATTGAACCGAAA CAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGCTCTGAAGTCTCTGAAAA TGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTTGGGGGGCTGAGCAACATGGAA GATGCTGCAGGAACTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGG AGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGAT TCAAGCTTCCTTGGCCTAAGCTTACTAAATACACTGCACATTGGGAACAACAGAGTCAGCTA CATTGCTGATTGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAACAATG AAATTTCCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGA CTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGC ATTGGAGCATCTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAC AAATGAAGAAACTGCAACAATTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTA AAATGGCTCCCACAGTGGGTGGCGGAAAACAACTTTCAGAGCTTTGTAAATGCCAGTTGTGC ATGATTTTCCCAAACCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCC AATTTGAGTTTCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCCAATGACTTTTGCTTGGAA AAAAGACAATGAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAG GTGGCGAGGTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAG GGGAAATATCAGTGTCATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCT TACAGTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGG CCATGGCACGCTTGGAGTGTGCTGTGGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAG CGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGA

Figure 101B

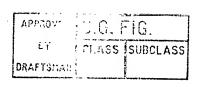
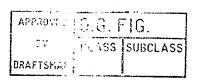


FIGURE 101B

From Figure 101A

ACAGTGCAGGAAGTATTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATTTTTG CGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCATTGCTGG AGGAAGCCCTCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGTAACCGÁGA GGCACTTTTTTGCAGCAGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCT GGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAG TGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATCGTTAGACGATGACG GATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGTGTGGTGGGCACGTCACTC GTGTGGGTGGTCATCATATACCACACAGGCGGAGGAATGAAGATTGCAGCATTACCAACAC AGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCATCTCAGGGAACGTTAGCTG ACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACCAGTTTGTCACATCTTCA GGTGCTGGATTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAG TGAAGCTGATGTGGAAGCTGCCACAGATCTGTTCCTTTGTCCGTTTTTTGGGATCCACAGGCC CTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCTTTTGAAACATATCATACAGGTTGC AGTCCTGACCCAAGAACAGTTTTAATGGACCACTATGAGCCCAGTTACATAAAGAAAAAGGA GTGCTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGT GGCCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATG AAAAATCTGTGTCTAAACAAGTCCTCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGT TGCCTCGAGTAATTCTTTCATGGGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATG CCTATTCAAGCTTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCAT AGAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGT CTTATGACTTGGACACA**TAG**ACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAG TGAACTTTTATTTAAAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAA GGATAAAAATGCTTTATTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTTAT ACTGGGAATGATGCTCATATAAGAATACCTTTTTAAACTATTTTTTAACTTTGTTTTATGCA AAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTATAATGC CAGATTTCTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCA TTTTTTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATT **TGAA**



MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP GYFDNLANTLLVLKLNRNRISAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM QRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE FCQKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLÖLKNNE ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLOGNAFSO MKKLQQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAOG GEVMEYTTILRLREVEFASEGKYOCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA MARLECAAVGHPAPOIAWOKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAON SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTER HFFAAGNOLLIIVDSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPOMTAPSLDDDG WATVGVVIIAVVCCVVGTSLVWVVIIYHTRRRNEDCSITNTDETNLPADIPSYLSSOGTLAD RQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP MYLKGNVYGSDPFETYHTGCSPDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISW PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA YSSFGQPSDCQPRAFYLKAHSSPDLDSGSEEDGKERTDFQEENHICTFKQTLENYRTPNFOS YDLDT

Signal sequence: amino acids 1-19

Transmembrane domain: amino acids 746-765

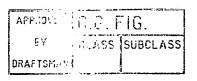
N-glycosylation site: amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459, 628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site: amino acids 826-830

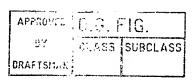
Casein kinase II phosphorylation site: amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268, 314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653, 671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962, 1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site: amino acids 607-615

N-myristoylation site: amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534, 612-618, 623-629, 714-720, 873-879



CCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAAC TGATTGTGCAAGAGAAGGAAGGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTÁACACAA ATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACCAGAGTTAGAĞČCGCGGG GGTTGGTGTTCTGACATAAATAATATCTTAAAGCAGCTGTTCCCCTCCCCACCCCCAA AAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAAGTATGTŤŒATTTTT CTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGGCTTTTTT AGGAAATTAATAATACATCTGCAAAGAAATTTCAGAGAAGAAAAGTTGACCGCGGCAGATTG AGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGATTTGTGCCTATGTTGACTAA CCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCTTAACCACCTGGATTTCCATCTGGAT GTTGCTGTGATCAGTCTGAAATACAACTGTTTGAATTCCAGAAGGACCAACACCAGATAAAT TATGA**ATG**TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAAC AGGGCCCTATTTGACCCCCTGCTTGTGGTGCTGCTGGCTCTTCAACTTCTTGTGGTGGCTGG TCTGGTGCGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAACCAGTTCAGCAAGGTGA TTTGTGTTCGGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCTGCTG AACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTT GGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTC TGGCGAACCTCAACACTCTGGAACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCT TTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTTGCGAAACAACCCCATTGAAAGCATCCC TTCTTATGCTTTTAACAGAATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGAC TTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACTTGAGGTATTTGAACCTTGCC ATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCT TTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAA AACTGTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAG TCACTAGTGGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCAC TCCCTTGCATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAACTGTAACTGTGACA TACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCGG TGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAG CTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGA ACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGTGCTCAGTGATGGTACGTTAAA TTTCACAAATGTAACTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAATTCCGTTG GGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTCTTAC TTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAA CAATGTGGGTCCCACTCCAGTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACAC CACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGACTGATATAAACAGTGGG ATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCATTGGGTGTTTTGTGGCCAT CACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGCACCATCGGC AAAACCATCACGCCCCAACAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGA GACACCCCATGGAAAGCCACCTGCCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTA TAACTCATACAAATCTCCCTTCAACCACAACAACAACAGTTAACACAATAAATTCAATACACA GTTCAGTGCATGAACCGTTATTGATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAA AAGAAAAGAAATTTATTAATTAAAAATTCTATTGTGATCTAAAGCAGACAAAAA



MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGIMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN
TTASATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence: amino acids 1-44

Transmembrane domain: amino acids 523-543

N-glycosylation site: amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 183-187

Casein kinase II phosphorylation site: amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site: amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243, 391-397, 422-428, 433-439, 531-537

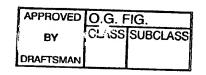


FIGURE 105A

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTG CTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGĆÁGCG CGAGGGAGGGCGCGCCGCGACGCGAGGGCGGCGTGCACCCTCGGCTGGAAGTTTGTGC CGGGCCCGAGCGCGCCGGCTGGAGCTTCGGGTAGAGACCTAGGCCGCTGGACCGCAT GGCGCGCTGGCCGACAGCGCGGCGGTCGCGGGGAACTCGGGCAGCCCTCTGGGGTÂGCC GCCGAGCGCCCATGCCCACTACCTGCCGCTGCCTCGGGGACCTGCTGGACTGCAGTCGTAA GCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCCTGGGTCGCTCGGCTGGACTTAAGTCACA ACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAA CTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGTCTCGGCAAATATTACACT TCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAGTTTCAGT CCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTCAGAGCTCCAAACTGCATTTCCAGCC CTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTT TGACAATTTGGCCAACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCC CACCCAAGATGTTTAAACTGCCCCAACTGCAACATCTCGAATTGAACCGAAACAAGATTAAA AATGTAGATGGACTGACATTCCAAGGCCTTGGTGCTCTGAAGTCTCTGAAAATGCAAAGAAA TGGAGTAACGAAACTTATGGATGGAGCTTTTTGGGGGGCTGAGCAACATGGAAATTTTGCAGC GAACTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCA GAAGCTCAGTGAGCTGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCC TTGGCCTAAGCTTACTAAATACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGAT TGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCCTG GACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTCC AAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCAT CTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAA ACTGCAACAATTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCC CACAGTGGGTGGCGAAAACAACTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAG CAAACCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTT TCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCCAATGACTTTTGCTTGGAAAAAAGACAAT GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGT

To Figure 105B

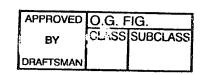
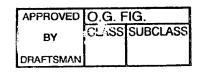


FIGURE 105B

From Figure 105A

GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATC AGTGTGTCATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCTTACAGTAAAT ATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCATGGCACG CTTGGAGTGTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCA CAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTT ATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGG AAGTATTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATTTTTTGCGGCCACTGT TGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCATTGCTGGAGGAAGCCCT CCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGTAACCGAGAGGCACTTTTT TGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAAATACA CATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGAGAACGTGCGCCTCAGTGTGATCCCC ACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCAC TCATCATATACCACACAGGCGGAGGAATGAAGATTGCAGCATTACCAACACAGATGAGACC TGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACCAGTTTGTCACATCTTCAGGTGCTGGAT TTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGAT GTGGAAGCTGCCACAGATCTGTTCCTTTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTT GAAGGGAAATGTGTATGGCTCAGATCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACC CAAGAACAGTTTTAATGGACCACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCA TGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACA TGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGT GTCTAAACAAGTCCTCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGT AATTCTTTCATGGGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAG CTTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAG ACTTGGACTCTGGGTCAGAGGAAGATGGGAAAGAAGGACAGATTTTCAGGAAGAAATCAC ATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGTCTTATGACTT GGACACA**TAG**ACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACTTTTÀ TTTAAAAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAT GCTTTATTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTTATACTGGGAATG ATGCTCATATAAGAATACCTTTTTAAACTATTTTTTAACTTTTGTTTTATGCAAAAAAGTATC TTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTATAATGCCAGATTTCTT TTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTTTAAAT AGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAAAAA AAAAAAAAAAAAAAAAAAAAA



MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLLDCSR KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT, LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY FDNLANTLLVLKLNRNRISAIPPKMFKLPOLOHLELNRNKIKNVDGLTFOGLGALKSLKMOR NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC OKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEIS. WTIEDMNGAFSGLDKLRRLILOGNRIRSITKKAFTGLDALEHLDLSDNAIMSLOGNAFSOMK KLQQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDF PKPOITVOPETOSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAOGGE VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA RLECAAVGHPAPOIAWOKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAONSA GSISANATLTVLETPSFLRPLLDRTVTKGETAVLOCIAGGSPPPKLNWTKDDSPLVVTERHF FAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA TVGVVIIAVVCCVVGTSLVWVVIIYHTRRRNEDCSITNTDETNLPADIPSYLSSOGTLADRO DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY LKGNVYGSDPFETYHTGCSPDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISWPS HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS SFGOPSDCOPRAFYLKAHSSPDLDSGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYD LDT

Signal sequence: amino acids 1-27

Transmembrane domain: amino acids 808-828

N-glycosylation site: amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site: amino acids 886-890

Casein kinase II phosphorylation site: amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site: amino acids 667-675

N-myristoylation site: amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern: amino acids 58-80, 65-87

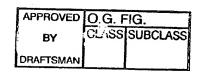


FIGURE 107A

CAAAACTTGCGTCGCGGAGAGCGCCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGA GCGCAGCTGAGACTGGGGGAGCGCGTTCGGCCTGTGGGGCGCCGCTCGGCGCGGGGCGCAG CAGGGAAGGGGAAGCTGTGGTCTGCCCTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGA-4 GCCCCTGGGTGGTCCCGTCCCTATCCCTCCTTTATATAGAAACCTTCCACACTGGGAAGGC AGCGGCGAGGCAGGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAGGCGCACAGCA GGTTCCATCAGCCCTGGCGCCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCC CAGAGCCGGGTGCTGCTCCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCT TGCCGTGAGGCCCCAGGATTTGGCCGAAGTGGCGGCCACAGCCTGAGCCCCGAAGAGAACG AATTTGCGGAGGAGCCGGTGCTGGTACTGAGCCCTGAGGAGCCCGGGCCTGGCCCAGCC GCGGTCAGCTGCCCCGAGACTGTGCCTGTTCCCAGGAGGGCGTCGTGGACTGTGGCGGTAT ACCAGCTGGAAAAGATCTACCCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAAC CTGCAAAACAACCGCCTGACTTCCCGAGGGCTCCCAGAGAAGGCGTTTGAGCATCTGACCAA CCTCAATTACCTGTACTTGGCCAATAACAAGCTGACCTTGGCACCCCGCTTCCTGCCAAACG CCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCTATGGGCTCACCTTTGGC CAGAAGCCAAACTTGAGGTCTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGCTGCC GGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCCTCATCCTGTCCAGCAACTTCCTGC GCCACGTGCCCAAGCACCTGCCGCCTGTACAAGCTGCACCTCAAGAACAACAAGCTG GAGAAGATCCCCCGGGGGCCTTCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAA CAACTACCTGACTGACGAGGGCCTGGACAACGAGACCTTCTGGAAGCTCTCCAGCCTGGAGT ACCTGGATCTGTCCAGCAACACCTGTCTCGGGTCCCAGCTGGGCTGCCGCGCAGCCTGGTG CTGCTGCACTTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCCG CCTTCCAGGGCCTCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTG CCCAGTGGCCTCGCCGCGTGCGCACCCTCATGATCCTGCACAACCAGATCACAGGCAT TGGCCGCGAAGACTTTGCCACCACCTACTTCCTGGAGGAGCTCAACCTCAGCTACAACCGCA CTGTCGGGCAACCGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAA GGTCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGGCGCTGGCGGGCATGGCTCAGCTGC GTGAGCTGTACCTCACCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCCTGGGTG

To Figure 107B

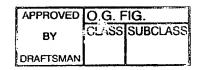
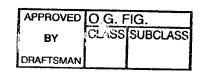


FIGURE 107B

_From Figure 107A

GACCTCGCCCATCTGCAGCTGCTGGACATCGCCGGGAATCAGCTCACAGAGATCĞCGGAGGG GCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACAACAAGATTAGTGCGGTGCCCGCCA GGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGG AGGAAGAGGAGGAGGAGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACC TAGGATGATGGACCGCCGGACTCTTTTCTGCAGCACACGCCTGTGTGCTGTGAGCCCCCCAC TCTGCCGTGCTCACACACACACCCAGCTGCACACATGAGGCATCCCACATGACACGGGCT GACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCCCACGGCCAGACACATGCACACA CATCACACCCTCAAACACCCAGCTCAGCCACACACACTACCCTCCAAACCACCACAGTCTC TGTCACACCCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCCTGC CCTGGCACACACGGCACCCATTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACA CCACACACACACATGCACAAGTCATGTGCGAACAGCCCTCCAAAGCCTATGCCACAGACA GCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCTGTCCATCTGTCCGTC AACTCACAAAAGCTGGCTTTTATTCCTTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTG $\tt CTGGCCTGGCCCACCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCC$ TCCCTGCCACGCCCTGGCAGGACACAGGCACTTTTCCAATGGGCAAGCCCAGTGGAGGCAGG ATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGGCAGGAGTGAAGCAGAGGTGATGGGG CTGGGCTGAGCCAGGGAGGAGGACCCAGCTGCACCTAGGAGACACCTTTGTTCTTCAGGCC TCTCAAAGCTGATTTTCTTGTTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGC AAAAAAAAA



MEGEEAEQPAWFHQPWRPGASDSAPPAGTMAQSRVLLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETLNLQNNRLTSRGLPEKAFEHLTNLNYLYLÄNNK
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSPQVHRDAFRKLRLLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEE

Signal sequence: amino acids 1-48

N-glycosylation site: amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site: amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site: amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341, 477-483, 498-502, 539-545, 548-554

Leucine zipper pattern: amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493, 535-557

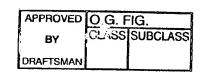


FIGURE 109A

GGGAGGGGCTCCGGGCGCGCGCAGCAGCCTGCTCCGGCCGCGCGCCTCGCCGCTGTCCT CCGGGAGCGCAGCAGTAGCCCGGGCGGCGAGGGCTGGGGGTTCCTCGAGACTCTCAGAGGG GCGCCTCCCATCGGCGCCCACCCCCAACCTGTTCCTCGCGCGCCACTGCGCCCCCCA GGACCCGCTGCCCAACATGGATTTTCTCCTGGCGCTGGTGCTGGTATCCTCGCTCTACCTGC AGGCGGCCGAGTTCGACGGGAGGTGGCCCAGGCAAATAGTGTCATCGATTGGCCTATGT GCCTGTGTGCCAACCACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTC ATCCTGGTTATGCTGGAAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGG CCCTGTAAGCACAGGTGCATGAACACTTACGGCAGCTACAAGTGCTACTGTCTCAACGGATA TATGCTCATGCCGGATGGTTCCTGCTCAAGTGCCCTGACCTGCTCCATGGCAAACTGTCAGT ATGGCTGTGATGTTGAAAGGACAAATACGGTGCCAGTGCCCATCCCCTGGCCTGCACCTG GCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCC TAGATTTAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCATAAAGGCTTCG ATCTCATGTATATTGGAGGCAAATATCAATGTCATGACATAGACGAATGCTCACTTGGTCAG TATCAGTGCAGCAGCTTTGCTCGATGTTATAACGTACGTGGGTCCTACAAGTGCAAATGTAA AGAAGGATACCAGGGTGATGGACTGACTTGTGTGTATATCCCAAAAGTTATGATTGAACCTT CAGGTCCAATTCATGTACCAAAGGGAAATGGTACCATTTTAAAGGGTGACACAGGAAATAAT AATTGGATTCCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCCTCCTAT CATTACCAACAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATTC CTACTCCACCACCACCACCACCACCACCAGACAGAGCTCAGAACACCTCTACCACCTACAACC CCAGAAAGGCCAACCACCGGACTGACAACTATAGCACCAGCTGCCAGTACACCTCCAGGAGG GATTACAGTTGACAACAGGGTACAGACAGACCCTCAGAAACCCAGAGGAGATGTGTTCAGTG GACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTCGGCAGC CAAAGCCCCAGGGGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCCTCATGCATTCAG GGGACCTGTGCCTGTCATTCAGGCACAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTG TTTGTGAGAAAACACGGTGCCCACGGAGCAGCCCTGTGGGGAAGAAATGGTGGCCATGGCTG GAGGCAAACACAGATCACCTTGCGAGGGGCTGACATCAAGAGCGAATCACAAAGA**TGA**TTAA AGGGTTGGAAAAAAGATCTATGATGGAAAATTAAAGGAACTGGGATTATTGAGCCTGGAGA AGAGAAGACTGAGGGGCAAACCATTGATGGTTTTCAAGTATATGAAGGGTTGGCACAGAGAG

To Figure 109B

APPROVED O.G. FIG.

BY CLASS SUBCLASS

DRAFTSMAN

FIGURE 109B

From Figure 109A

GGTGGCGACCAGCTGTTCTCCATATGCACTAAGAATAGAACAAGAGGGAAACTGGCTTAGACT AGAGTATAAGGGAGCATTTCTTGGCAGGGGCCATTGTTAGAATACTTCATAAAAAAAGAAGT GTGAAAATCTCAGTATCTCTCTCTCTTTTCTAAAAAATTAGATAAAAATTTGTCTATTTAAGA TGGTTAAAGATGTTCTTACCCAAGGAAAAGTAACAAATTATAGAATTTCCCAAAAGATGTTT TGATCCTACTAGTAGTATGCAGTGAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAAT TTAGGCATTTCCCTCTTGACCTCCTAATGGAGAGGGGATTGAAAGGGGAAGAGCCCACCAAAT GCTGAGCTCACTGAAATATCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAAAGGAA ACTATTTATTCCAAATGAGAGTATGATGGACAGATATTTTAGTATCTCAGTAATGTCCTAGT GTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCCTTTCATTTGTTCAATGGA TGATGTTTCAGATTTTTTTTTTTTTAAGAGATCCTTCAAGGAACACAGTTCAGAGAGATTTT CATCGGGTGCATTCTCTCTGTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGC CCTGCCCCACACCGGCAGACCTTTCCTTCACCTCATCAGTATGATTCAGTTTCTCTTATCAA TTGGACTCTCCCAGGTTCCACAGAACAGTAATATTTTTTGAACAATAGGTACAATAGAAGGT AGTAACGCCAGAATATATGGCTGTAGATCCATTTTTAATGGTTCATTTCCTTTATGGTCATA TAACTGCACAGCTGAAGATGAAAGGGGAAAATAAATGAAAATTTTACTTTTCGATGCCAATG ATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTTGTTTATTA TTTAATGTTTTCTAAAATAAAAATGTTAGTGGTTTTCCAAATGGCCTAATAAAAACAATTA TTTGTAAATAAAAACACTGTTAGTAAT

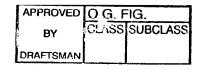


FIGURE 110

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKEKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDPQKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence: amino acids 1-17

N-glycosylation site: amino acids 273-277

Casein kinase II phosphorylation site: amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site: amino acids 199-206

N-myristoylation site: amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242, 421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site: amino acids 104-116, 186-198, 231-243

Cell attachment sequence: amino acids 382-385

EGF-like domain cysteine pattern signature: amino acids 75-87

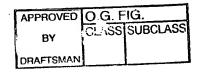
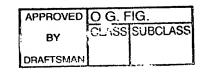


FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCTTTAGATTGTGA CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACC AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCCT GATGAAGGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACTCTATCTGCCAGTCA GAAGATACAAGTCACGGTTGATGATCCTGTCACAAAGCCAGTGGTGCAGATTCATCCTCCCT CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC TCCCCAAAACAATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT GCCTGGTGAGGAACCCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTAT GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCCAACACCTACT CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTT GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC CGGCAGGCAAGATGAAACTCATTTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG CACAGAAAGGAAAATCATTGTCACCTTTAGCAAGTATAACTGGAATATCACTATTTTTGATT ATATCCATGTGTCTTCTTTCCTATGGAAAAATATCAACCCTACAAAGTTATAAAACAGAA ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG ATTCCAAGCAGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT $\tt GTATGAAGTTATTCAGCACATCCCTGCCCAGCAGCAGCAGCCATCCAGAG{\color{red}{\textbf{TGA}}} ACTTTCATGG$ GCTAAACAGTACATTCGAGTGAAATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAGT ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCTTTACA TGCAGAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTTCAGCATATACACAATGTCTT GTGCAACAGAAAACATGTTGGGGAAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG GGAGAACGAAAGTGACAGGGGTTTCCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA ATTAGTTCTACTCTACACTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA TGTGGAAACTTTACATTGTTCGATTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTA AΑ



MWLKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPHTMP
KYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQKIQVTV
DDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFSPQNNTLHIA
PVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTVDLGEAILFDCSA
DSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNITGRQDETHFTYIITSV
GLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQKLEGRPETEYRKAQTFSGH
EDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTVYEVIQHIPAQQQDHPE

Signal sequence: amino acids 1-18

Transmembrane domain: amino acids 341-359

N-glycosylation site: amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208, 276-280, 308-312

Casein kinase II phosphorylation site: amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site: amino acids 272-280

N-myristoylation site: amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237, 239-245

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 7-18

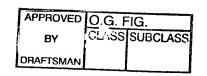
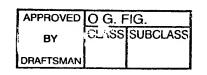


FIGURE 113

GCTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTCGCGTCATCACGGACGAGA ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT... TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAA TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC TTCCTACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCGTTTCATCATG TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC AGATTGCCTTTGTCCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCTTCAAAAAAAT TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCC**TAG**TTAAATTTTATAG AACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA CATTCAGAACATAAAAGCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATG GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGT TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAATTTACATTTCCCAAGTATTGCATTAT TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTTCTCTG TTTCACTGTGTGAAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTGTCTCAAG AAATGTGTATTTCAGTGACAATTTCGTGGTCTTTTTAGAGGTATATTCCAAAATTTCCTTGT TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTC GTTTCAAACTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAAATT TTGGCCACTTTTTCAGATTTTACATCATTCTTGCTGAACTTCAACTTGAAATTGTTTTTT TTTCTTTTTGGATGTGAAGGTGAACATTCCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTA TTTTACATTTTGAAAATTCAAAGAAGCTTAATATAAAAGTTTGCATTCTACTCAGGAAAAAG CATCTTCTTGTATATGTCTTAAATGTATTTTTGTCCTCATATACAGAAAGTTCTTAATTGAT TTTACAGTCTGTAATGCTTGATGTTTTAAAATAATAACATTTTTTATATTTTTTAAAAGACAA ACTTCATATTATCCTGTGTTCTTTCCTGACTGGTAATATTGTGTGGGGATTTCACAGGTAAAA GTCAGTAGGATGGAACATTTTAGTGTATTTTTACTCCTTAAAGAGCTAGAATACATAGTTTT CACCTTAAAAGAAGGGGGAAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC AATTTCTGTAATGTCCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAAATATTGTACCATT AAAGAGTTTGGATGTAACTTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAAACCT



MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACONL QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence: amino acids 1-26

Transmembrane domain: amino acids 182-201

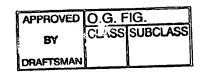
Casein kinase II phosphorylation site: amino acids 68-72,

119-123, 128-132, 247-251, 257-261

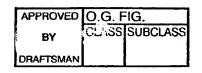
Tyrosine kinase phosphorylation site: amino acids 107-115

N-myristoylation site: amino acids 20-26, 192-198

Amidation site: amino acids 25-29



GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTTAACTAATTCAACAAACGGGACCCTT CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG AAGGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC ATTGCTGATGGCCTGGTTTGGTGTCCTGAGCTGTGTGCAGGCCGAATTCTTCACCTCTATTG GGCACATGACTGACTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTAĆATC CTTGTGGAGGAAGCCAAGCTTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCCTGTGAATGCCTACAAACTGG TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCCTGCAGGACTCAGCTGCA GGTTTTATCGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA GAGGGGAACTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG AAAGCAGCTTGATGCCGGGGAGGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCCTGCTC TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGCA TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGGATGTTTACGAGAGCCTCTGTCGTGGG GAGGGTGTCAAACTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA TCGTCAGGTACTACGATGTCATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA CCTAAACTTGCACGAGCCACCGTTCGTGATCCCAAGACAGGAGTCCTCACTGTCGCCAGCTA CCGGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATC GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTG GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT TGAGACCTTGTGGATCAACAGAAGTTGAC**TGA**CATCCTTTTCTGTCCTTCCCCTTCCTGGTC CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCCTTTGTATGTTCCTATCAGGCT GATTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT GTGACTGAAGTCCCAGCCCTTCCATTCAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT



MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPSHERAGGNLR
YFEQLLEEEREKTLTNQTEAELATPEGIYERPVDYLPERDVYESLCRGEGVKLTPRRQKRLF.
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYR
TRHAACPVLVGCKWVSNKWFHERGOEFLRPCGSTEVD

Signal sequence: amino acids 1-17

N-glycosylation site: amino acids 115-119, 264-268

Glycosaminoglycan attachment site: amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 477-481

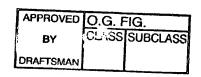
Casein kinase II phosphorylation site: amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270, 346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site: amino acids 71-80, 489-496

N-myristoylation site: amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 8-19

Leucine zipper pattern: amino acids 213-235



TGAAATTGATTGTTTCATTTATTACCGTTTTTGGCTGGGGGTTAGTTCCGACACCTTCACAGT TGAAGAGCAGGCAGAAGGAGTTGTGAAGACAGGACAATCTTCTTGGGGATGCTGGTCCTGGA AGCCAGCGGGCCTTGCTCTTTTGGCCTCATTGACCCCAGGTTCTCTGGTTAAAACTGAA AGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCCCCTGGĞGCAC TTCCCCTCATCTTAGGGCTGTCTCTGGGGTGCAGCCTGAGCCTCCTGCGGGTTTCCTGGATC ~ CAGGGGGAGGAGAAGATCCCTGTGTCGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCC AGATTCGAGAGCTCGGCTAGACCAAAGTGATGAAGACTTCAAACCCCGGATTGTCCCCTACT GGCTCCCGTGAGCGGTTGCTGGTGGCTGTCCTGACCTCCCGAGCTACACTGTCCACTTTGGC CGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCACTGGGCAGC GGGGGGCCCGGGCTCCAGCAGGGATGCAGGTGTCTCATGGGGATGAGCGGCCCGCCTGG CTCATGTCAGAGACCCTGCGCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTT CATCATGCAGGATGACACATATGTGCAGGCCCCCCGCCTGGCAGCCCTTGCTGGCCACCTCA GCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGGTTCATTGGCGCAGGCGAGCAGGCC CGGTACTGTCATGGGGGCTTTGGCTACCTGTTGTCACGGAGTCTCCTGCTTCGTCTGCGGCC ACATCTGGATGGCTGCCGAGGAGACATTCTCÁGTGCCCGTCCTGACGAGTGGCTTGGACGCT GCCTCATTGACTCTCTGGGCGTCGGCTGTGTCTCACAGCACCAGGGGCAGCAGTATCGCTCA TTTGAACTGGCCAAAAATAGGGACCCTGAGAAGGAAGGGAGCTCGGCTTTCCTGAGTGCCTT CGCCGTGCACCCTGTCTCCGAAGGTACCCTCATGTACCGGCTCCACAAACGCTTCAGCGCTC TGGAGTTGGAGCGGGCTTACAGTGAAATAGAACAACTGCAGGCTCAGATCCGGAACCTGACC GTGCTGACCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTCAC ACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCCT GTGCAGATGGGGCTCCCAAGTGCCCACTACAGGGGGGCTAGCAGGGCGGACGTGGGTGATGCG TTGGAGACTGCCCTGGAGCAGCTCAATCGGCGCTATCAGCCCCGCCTGCGCTTCCAGAAGCA GCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCACGGGGCATGGAGTACACCCTGGACC TGCTGTTGGAATGTGTGACACAGCGTGGGCACCGGCGGGCCCTGGCTCGCAGGGTCAGCCTG CTGCGGCCACTGAGCCGGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGT GCAGCTGGTGCTGCCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTTCCTCGAGGCGT TTGCAGCCAATGTCCTGGAGCCACGAGAACATGCATTGCTCACCCTGTTGCTGGTCTACGGG CCACGAGAAGGTGGCCGTGGAGCTCCAGACCCATTTCTTGGGGTGAAGGCTGCAGCAGCGGA GTTAGAGCGACGGTACCCTGGGACGAGGCTGGCCTGGCTGTGCGAGCAGAGGCCCCTT CCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCCTGTGGACACTCTCTTCCTT ACCACCGTGTGGACAAGGCCTGGGCCCGAAGTCCTCAACCGCTGTCGCATGAATGCCATCTC TGGCTGGCAGGCCTTCTTTCCAGTCCATTTCCAGGAGTTCAATCCTGCCCTGTCACCACAGA TCCCGGGGGGCTCCTATAGGGGGGAGATTTGACCGGCAGGCTTCTGCGGAGGGCTGCTTCTA CAACGCTGACTACCTGGCGGCCCGAGCCCGGCTGCAGGTGAACTGGCAGGCCAGGAAGAGG AGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTTCCTCCGGTTCTCAGGGCTCCACCTC TTTCGGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCT CAGTGAAGAACTCTACCACCGCTGCCGCCTCAGCAACCTGGAGGGGCCTAGGGGGCCGTGCCC AGCTGGCTATGGCTCTCTTTGAGCAGGAGCAGGCCAATAGCACT**TAG**CCCGCCTGGGGGCCC TAACCTCATTACCTTTCCTTTGTCTGCCTCAGCCCCAGGAAGGCCAAGGCAAGATGGTGGAC AGATAGAGAATTGTTGCTGTATTTTTTAAATATGAAAATGTTATTAAACATGTCTTCTGCC

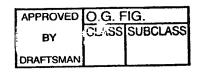


FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTLDLLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPLL
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAQLAMALFEQEQANST

Signal sequence: amino acids 1-15

Transmembrane domain: amino acids 489-507

N-glycosylation site: amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 319-323, 464-468

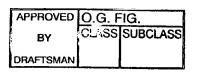
Casein kinase II phosphorylation site: amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389, 399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site: amino acids 736-743

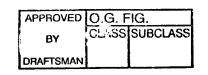
N-myristoylation site: amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550, 558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 14-25

Cell attachment sequence: amino acids 247-250



CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGCTGCGCTTTCCTGTCCCCAAGCC -GTTCTAGACGCGGGAAAA**TG**CTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAÄATAGAA TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAÂATTTCA GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAÄÄÄCC CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG AGTTCTTCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATG TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACTG AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT CAATATCCCAGAAAAGTGTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC ATCAGATGCATGTGATGTATGGGGTATACCGCCTTAGGGCATTTGGGCATATTTTCAAT GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAAGTGGTAGAAAAGCG TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACTACATATCCAA TACAGCTGTATGTTTCTTTTTCTTATTTGGTGGCACTGGTATAACCACACATTAAAG TCAGTAGTACATTTTTAAATGAGGGTGGTTTTTTTTCTTTAAAACACATGAACATTGTAAATG GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCCACATATTTTTGCTGATTGGTT AAAAAATTTTAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT TGTGATTAAAGTAAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT AAGCCTCCCCAAGTTCCAATGGATTTGCCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA ATTAAAGTGAAAGTTGAAAAAT



MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSGDLEYWGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL

Signal sequence: amino acids 1-33

N-glycosylation site: amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 319-323, 464-468

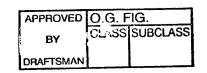
Casein kinase II phosphorylation site: amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389, 399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site: amino acids 736-743

N-myristoylation site: amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550, 558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 14-25

Cell attachment sequence: amino acids 247-250



AAAAAGAGAGAGAGAAAAAAAAACCAAAGAGAGAGAAAAA**ATG**AATTCATCTAAATCAT CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTCTCCCAAATGTTCTTATGGACTGTTGCT GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTEGCAT CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTCACAGAGCTCTCCTGCT ACAATTATGGATCAGGTTCAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC AGCTGCTACTTCTTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAACTGCTCAGC CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA AACCTAAAATGAGAGAGTTTTTTTTTGGACTGTCAGACCAGGTTGTCGAGGGTCAGTGGCAA TGGGTGGACGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGA ATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTG AACAAAGGAAAATCTCTT**TAA**GAACAGAAGGCACAACTCAAATGTGTAAAGAAGGAAGAGCA AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC AAAAA

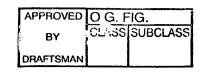


FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS
NPRONWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence: amino acids 1-42

N-glycosylation site: amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site: amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site: amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site: amino acids 27-38

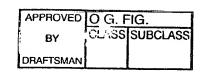


FIGURE 123A

GGGACTACAAGCCGCGCGCGCGCTGCCGCTGGCCCCTCAGCAACCCTCGACATGGCGCTGAGG CGGCCACCGCGACTCCGGCTCTGCGCTGGCTGACTTCTTCCTGCTGCTGCTTTTCAG GGGCTGCCTGATAGGGGCTGTAAATCTCAAATCCAGCAATCGAACCCCAGTGGTÄCAGGAAT TTGAAAGTGTGGAACTGTCTTGCATCATTACGGATTCGCAGACAAGTGACCCCAGGÃTCGAG TGGAAGAAATTCAAGATGAACAAACCACATATGTGTTTTTTGACAACAAAATTCAGGGAGA CTTGGCGGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGA GAGACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAG TGTACCAGTAGGCAAGATGGCAACACTGCACTGCCAGGAGAGTGAGGGCCACCCCGGCCTC ACTACAGCTGGTATCGCAATGATGTACCACTGCCCACGGATTCCAGAGCCAATCCCAGATTT CGCAATTCTTCTTTCCACTTAAACTCTGAAACAGGCACTTTGGTGTTCACTGCTGTTCACAA GGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGG CTTGCTGTACTGGCCCTGATCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCAT CAACAATAAACAGGATGGAGAAAGTTACAAGAACCCAGGGAAACCAGATGGAGTTAACTACA TCCGCACTGACGAGGGGGGGCGACTTCAGACACAAGTCATCGTTTGTGATC**TGA**GACCCGCGG TGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAAGGCA GCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAGAAGCTTTTCGTTTTGGCCAA AGTTGACCACTACTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCCTCAAGATG GACCCGGTAAATATAACCACAAGGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCTAA TCTGTTTCTGGCCTGATTCCCGCATGAGTATTAGGGTGATCTTAAAGAGTTTGCTCACGTAA ACGCCCGTGCTGGGCCCTGTGAAGCCAGCATGTTCACCACTGGTCGTTCAGCAGCCACGACA GCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCAG AAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCCACAGACACCACCGCAGTTTCTTCT TAAAGGCTCTGCTGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTTGGATCAGCATTT TGTAAAAACAACCAAAATCAGGAAGGTAAATTGGTTGCTGGAAGAGGGGATCTTGCCTGAGGA ACCCTGCTTGTCCAACAGGGTGTCAGGATTTAAGGAAAACCTTCGTCTTAGGCTAAGTCTGA AATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTTTACATCTAAAT TTTTGCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAAACTGTAAATATATT GTCATACAATGTTAAATAACCTATTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAG CTACTAGTGTTAAATTGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCA

To Figure 123B

APPROVED O.G. FIG.

BY CLASS SUBCLASS

DRAFTSMAN

FIGURE 123B

From Figure 123A

TGGAAGTTTACTGTGATGTTCCTTTTCTCACACAGTTTTTAGCCTTTTTCACAAGGGAACTC ATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTTTAAAAATTCCAGTTAAGCAAT GTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACTGCCTCTŤC ${\sf AGATGCCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGC}$ TGTCTGCCAGGAGGCCCTGCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCCAGTGAGCTTTA CTCACGTGGCCCTTGCTTCATCCAGCACAGCTCTCAGGTGGGCACTGCAGGGACACTGGTGT TGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTAAAAGA AAATGGATCCCACTGTTCCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTCG CATTTCAAAACAACCATGATGGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTCAGGTGG AGCAGCCAGGTGAAAGGCCTGGCGGGGGAGGAAAGTGAAACGCCTGAATCAAAAGCAGTTTTC TAATTTTGACTTTAAATTTTTCATCCGCCGGAGACACTGCTCCCATTTGTGGGGGGGACATTA GCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCTGC CGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACT GTGTGCCTGGAGAATGGCTCTCACTACTCACCTTGTCTTTCAGCTTCCAGTGTCTTGGGTTT TTTATACTTTGACAGCTTTTTTTTAATTGCATACATGAGACTGTTGTTGACTTTTTTTAGTTA TGTGAAACACTTTGCCGCAGGCCGCCTGGCAGAGGCAGGAAATGCTCCAGCAGTGGCTCAGT GCTCCCTGGTGTCTGCATGCATCCTGGATGCTTAGCATGCAAGTTCCCTCCATCATTG CCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTCACGCTCCAGCCTCC TTCTTGGTTGTCATAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACCTT CTACACTAGTGCCATGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGG AAGTAGCTGCCTATAACTGAGACTAGACGGAAAAGGAATACTCGTGTATTTTAAGATATGAA ACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTTGTTTAACCTCATTTAT AAAAGCTTCAAAAAAAACCCA

APPROVED O.G. FIG.

BY CLASS SUBCLASS

DRAFTSMAN

FIGURE 124

></usr/segdb2/sst/DNA/Dnasegs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK EIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Signal peptide: amino acids 1-30

Transmembrane domain: amino acids 243-263

N-glycosylation sites: amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 107-110

Casein kinase II phosphorylation site: amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site: amino acids 69-77

N-myristoylation sites: amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267